GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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July 30, 2004, 14:16:25; Search time 3640 Seconds (without alignments) 7251.623 Million cell updates/sec
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Gapop_60.0 , Gapext 60.0
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RS Wing, R.A., Yu, Y., Soderlund, C., Kim, H., Rambo, T., Saski, C., Currie, J., Collura, K., Minx, P., Du, H. and Thurmond, S.K.

Direct Submission

AL Direct Submission

AL Submitted (17-25P-2002) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA

On Sep 13, 2002 this sequence version replaced gi:22532548.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality as compressions and repeats; all regions were covered by more than one plasmid subclone; and the assembly was confirmed by restriction one plasmid subclone; and the assembly was confirmed by restriction digest. The following areas contain Th tandem repeats: 5185-5280 (12-48 pairs), 6500-6589 (11-45 pairs), 11108-11153 (23 pairs), 138956-139033 (39 pairs) and 139799-139886 (19-44 pairs).

Solly, 97860-100004, 118518-120649 and 1008575-112108. There is only a PCR read covering 18101-18204. Bases found in these locations are below threshold: 30629-30668 and 1008575-112108.

Fivery attempt has been made to resolve these areas and future attempts will be made as new techniques arise. There is only overlagn covering 120649-120926 and 141813-141908 The nucleotide sequence of this BAC clone was generated by combining Monsanto, Syngenca and Arizona Genomics Institute sequencing data. The assembly overlagp from base 11590-153510 with OSJNBa0013721 (accession #AC079843). The overlap is from base 1-40920 on Colling.
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YMCDPCADGYGRBNWPDSGEDVHGHIIGYGRFWGSTCWVKWHGABGEGSGSAAANRSGAHN
YMCDRADGYGRBNWPDSGEDVHGHIIGYGRFWGDAGARREDGAGARRSGAHN
YMCGCKAKHTKLSYTLDLMKLKASSGWTDKSFTDLLGILKAMLPVENTLPEMTYGAKQV
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GROVGKKSLISHVCNDBRIRBSYRSBILYINGDSSGGSIAHARKFRMERILIYGRSYTDII
GENDWYNPYSYVSQMTGGSKVVIISRIENLARFCTAKAVHLNSLSQEEVSYLFKMLA
TDQXDHPKMVSVANDLAVVLGGSLIIANMISDMLRRNHNVHFWLRILRRFERMVKNNF°
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/product="Putative_retrotransposable_elements_INP2"
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/mol_type="genomic DNA"
/sub_species="(japonica cultivar-group)"
/db_ref="taxon:39947"
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/note="Hypothetical protein"
complement (join(2435. .2524,2625. .3620))
/gene="OSJNBb0004A06.2"
/codon_start=1
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/note="Simple Sequence Repeat (TA)n"
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/protein_id="AAN11186.1"
/db_xref="G1:22953953"
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Continuation (21 of 24) of AC145127 from base 2000001 (AC145127 Oryza sativa (japonica
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Oryza sativa (japonica cultivar-group)
Bukaryota, Virdiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Subjurited (19.00)

Ning,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H.-R., Rambo,T., Saski,C., Henry,D., Oates,R. and Simmons,J.

Direct Submission

Loundited (19.NOV-2001) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA

3 (bases 1 to 153310)

Submitted (19.NOV-2001) Clemson University Genomics Institute, Saski,C., Henry,D., Oates,R. and Simmons,J.

Direct Submission

Loundited (19.NOV-2002) Clemson University Genomics Institute, Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA

4 (bases 1 to 153310)

Submitted (19.NOV-2002) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, Az 85721, USA

Submitted (19.NOV-2002) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, Az 85721, USA

Submitted, Nov. Soderlund,C., Kim,H., Rambo,T., Saski,C., Currie,J., Collura,K. and Thurmond,S.K. and Thu
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Oryza sativa (japonica cultivar-group) chromosome 10 clone
OSJNBb0004A06, complete sequence.
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Submitted (105-MAY-2003) The Institute for Genomic Research, 9712

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Medical Center Dr. Rockville, MD 20850, USA

This is the pseudomolecule for rice chromosome 10, which was constructed by resolving discrepancies between overlapping BACs, trimming the overlap regions, and linking the unique sequences to form a configure sequence. Genes in individual BAC clone were identified by a combination of several methods: Gene prediction programs, searches of the complete sequence against a peptide database and EST databases. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction proteins. Genes without significant predicted by more than two gene prediction proteins. Genes modificed by tRNAscan-SE (Sean Eddy, http://genome.wistl.edu/eddy/tRNAscan-SE).
TLVYDLWTFGPRREIASSIAELKVRAQLIADRRIRYGVENPNTQKGKGPPDATSYDIA
BOLASHELGMNEPVGMEKANKDLEBWFDGTAGCBFAVVSI 1VGFGGVGKTTIAMALYK
KVWYQFDCRAWTWSQNYDLDAULADILKQIDPDYRQQCSSKTGTSBNIKTLARFGSK
KKRDVQRTGSLRQSSPRSIBETSNLKRIETTDNXLESQIKKLLDKKRCVHPSIHLSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AE017053 303511 bp DNA linear PLN 06-JUN-2003 Oryza sativa (japonica cultivar-group) chromosome 10, section 7 of 77 of the complete sequence.
AE017053 AE016959 AE017053.1 GI:31430010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <1. 79862
/note="Chromosome Sequence Derivation: nucleotide sequence
in this region was derived from BAC clone OSJNBD0072F04
(GB.AC092553)."
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/locus tag="OSJNBb0072F04.10"
/locus tag="OSJNBb0072F04.10"
complement(<6121. .>7701)
/locus_tag="OSJNBb0072F04.10"
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 303511)
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/organism="Oryza sativa (japonica cultivar-group)"
/mol type="genomic DNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                In-depth view of structure, activity, and evolution of rice chromosome 10 Science 300, 1566-1569 (2003)
                                                                                                                                                                                                                                                                         3.4%; Score 21; DB 8; Length 153510;
100.0%; Pred. No. 1.9;
cive 0; Mismatches 0; Indels 0
                                                                                                                                                       26913. .27062
/note="Similar to Tourist_Oll MITE element"
complement(27190. .27338)
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/chromosome="10"
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                                                                                                                                                                                                                                                                                                                                                                                                            340 CAAGTACTTCATGCTGTTGGT 360
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SLNLDGVTRILDCCYNNLPGYLRTCLLYLAIFPKGHKISRKLISRRNLAEGFWNAKQ
THABEVALSSYPHILRRKLIRPEERSONGKLKTPQVHDWVLDYLVTKAREENPITVVG
GHLMMIAPSNNKVNBELMGASSSKHGOSTKGMTLSQVRSLTVPGSLTQLPFFRANDRI
IQVLDFQGLKGFKNRHMKHICKMFVLKYLSLRGTDITHVPPTIVKLEYLETLDIRETR
VKELFKEVGQLKLISRILGGSSVHKNPRKGLRLPQEKSKKQQHKSMLTYDDKEYEGMKAL
RILGGIKIDETTAVAGLHQTGLKKLITYTKLKLNPEEPGTRKILTELRSSIEYLCSCG
LQTLAINBEGQSNFINSLGNNSAPPRYLVALELSGMLKKPPGMIKTLTELRSSIEYLCSCG
LQTLAINBEGGSNFINSLGNNSAPPRYLVALELSGMLKKPPGMIKTLTELRSSIEYLLSLITLSLITSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /trānslation="MNLNNVGKKGLITDHANNKKQKRKKEKGNRSDWHGSTKDTIPFM
GDADFNHADEFGVVDGVACEGTQMAPALLLLCPHQQLMQIQSKCCYYTSSASSTGGGR
GQRAWAMVAIWRPPADKGGTAAADEDEGCWLLRIARQRGADRQRWKGSRWRPWAEERQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TQWNLQCSSIKCNIETIWPWGGISLHLLQNRQDVIFRRDFRGRKNYIIVILILRRSG
ICIGALKEIPKPPIFKHERSFRPPVLRIENGNDGSMITLQHGQVINSGIWIIKTPFH
CKTSVQPFQNQILTILLLIGPSGPSBAFLDMEESNKNSIVEKFRQHFSSPQFKNIQBQ
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ASMKAFLLDLAREDPDNRKKHWMKQIRDMAYDCEDCIDDFAHRLPNDSLDAKCCPWIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APFVVELASRSRRRDGLSPVPTTRSSYSLLLTGQEALWQEYRQKVSAWVTESRSLIGS
SLARIQAESFCSGRNRNGKGSIKFILRIKOLFVDESHELFLNRHDKFLVCEASKSKSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QKQOERĞSGTSÖSLMPKLDWKKASEKALTLACGSTVQGPPSQAVHTTTASKQCEKÖDK
EPIMQSTPEVGTEEMLVHGSTVKKKLVSSTIEDHVSCNSKNVNTVGKVHQMEPIQSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MGRGGTEGRSSGAGSGHPRAPVAGGKEREEEVASGLPTLSLPVE"
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RSRIIVTSRPQAVGSTCCRPENKDLLYPISFLSPRDSKELFNRSVSESKSTKDRHKVQ
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EEDKQTAQINDLLVRDLKDSTEGLKVIIDHTFTS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10975. .11020
// note==.5imple.Sequence Repeat (AT)n"
/pote==.05imple.potence Repeat (AT)n"
/gene="OSJNBb0004A06.4"
/pote=="Contains similarity to disease resistance protein"
/complement(ioin(19977. .21480,22331. .22551))
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/gene="OSJNBb0004A06.5"
/note="Contains similarity to disease resistance protein"
complement (24383. .25405)
                                                                                                                                                                                                                                                                                                                                                                                                                                note="Unknown protein"
loin(8249. .8785,9076. .9120,9930. .10065,11299. .11387,
10308. .11850,12602. .12789,13220. .13423,14642. .15154)
/gene="OSJNBb0004A06.3"
'note="Similar to Oryza sativa gene, repeat sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="Putative disease resistance protein"
protein id="AAN11188.1"
db_xref="G1:22953955"
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                                                     5518. ...5539
/note="Simple Sequence Repeat (AT)n"
5542. ..5575
/note="Simple Sequence Repeat (AT)n"
5602. ..5627
/note="Simple Sequence Repeat (AT)n"
                                                                                                                                                                                                                                                                                                          6368. .6457
/note="Simple Sequence Repeat (TA)n"
8249. .15154
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/note="Simple Sequence Repeat (AT)n"
10560. .10589
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                                                                                                                                                                                                                                              5724, .5745
/note="Simple Sequence Repeat
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db_xref="GI:22953956"
                                                                                                                                                                                                                                                                                                                                                                                                        gene="OSJNBb0004A06.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JVHRVSPSASAHQNRFLT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
                                 Micropan-1"
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/locus tag="OSCINBb0072F04.15"
/note="contains similarity to transposase"
/note="contains transportations"
/note="c
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/locus tag="OSJNBb0072F04.16"
complement (join(48333. .48348,48499. .48586,49139. .52859))
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/locus_tag="OSJNBb0072F04.14"
/note="contains similarity to copia type pol polyprotein"
complement (join(<25322. . 26796,27148. .27678,27724. . .27814,
28019. . .28279,28375, .28542.29526. .>29537))
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LAAKFDKDVMFWHRRLGHVGFDHLTRLSGLDLVRGLPKLKKNIDLDEAFQHFRGLFLR
LDLEFPGSLKRIRSDNGGLEHEFSSPRVPQQNGVVERKYRVLVEMARMMLDEYKTPKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FWARBINTACYISNRVFLRSKLGKTSVELRFGRQPKVSHLRVLSCKCFVLKSGNLDKR
BARSTDGLFLGYPAHSRGYRVLILETNKIIETCEVSFDBASPGTRPDIAGTLSGVQGG
DGRIFBDESEDDNNDEVGSAELENFERNKVWTFVEPPSEHNIFGTKWVFKNKQNBDGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IVRNKTRLVAQGETQVEGLDFDETFAHVARVEAIRLLLAFAISKGFKLYQMDVKSDFL
NGFIQEVYVKQPPGFENPEPPNHVFKLSKALYGLKQAPRAMYDRFKNFLLAKGFSMG
KVDKTLFVLKHGDNQLFVQIYVDDIIFGCSTHALVVEFAETMRREFEMSMMGELSYFL
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RSMIGSLLYLIASRLDIQLAMCLYTRFPASSPRASHRQAIKRIMKYLMHTLEFGIWYST
SSSICLGKYSDTDFGGCRIDKETSGICHFLGTSLIAMSRKQSSVAGSTSSESYVAA
ASCCGGLLMLLSTLKYSLTFEKYPLFCDNTSAINIAKNPVQHSRTHHINICFHFLRD
HVEKGDVELQFLQKMLQLADIFNKPLDSNHFAFLRGELGIIHPFGMV"
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SLPRQKTPNQPQPSQKSPSTGPIRKKTPTPSASQKGGSSGMERLPHSKSKLVPNPTT
SLPKKYGSSTITSLLGPKKPEBRAIPIPKVIEHTKCAQPRLPPKPISDFRTLEKSE
MOSSSRELFLDKKASDSPAAFCKSVDLKSLDDIDNLDKABVLLSSNNDDPWRCSYQCRS
LDRKIAFLDPRAVNPNNQLSKEKEIDDYLFNALVKQNGYDHILLPYLSHHHWILFVIN
                                                                                                                                                                                                                                                                                                                              complement (join (25322. '26796,27148. .27678,27724. .27814,
28019. .28279,28375. .28542,29526. .29537))
/locus_tag="cSJNBb0072F04.14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDDSKICVYDSLRKGTDNYQTIMNALNRAYVKYRRSKRTYGRCAIDATSFRIFENQYI
YRQPALTNLCGMYVMWYMLCFVESGHLLPRNAEKLGLETSEMLPHVFTALTD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note="contains similarity to NBS LRR type resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/producis="putative copia-type pol polyprotein"
/protein id="AAP51986.1"
/db_xreff="GI:31430015"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="putative transposase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  locus_tag="OSJNBb0072F04.16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . >52859)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (<48333.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .>42847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <32428.
                                                                                                                                            mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDDHCCSWIEVLGSVEINVANKTAAIBORVTSMACSPSSVPDWDSGNQGWIDVLSSVS
ISIAKKLETATAADNVSSECPAKWYRAMACSPSSVPDWDSDQGWIDVLGASPDVVAAB
FEDVAAADDISGQAVGSIVVGVGSSEQSVVVENQEDBFTSLSSCSERVLLVGVHAAD
NNAABSKAGIKRCSNFSC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (<10528. .>12105)
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/note="Contains similarity to NFK1 related protein kinase"
complement (<10528. .>12105)
/locus_tag="OSJNBb0072F04.11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLKKEVVKATWVS PTSALDAAALWESTTSSTDDBEADDWSNSPTGRIIAMASSGGO
TLPDWDSDDHGWIEVLGTVSINIAKKKTAAAEDYEASESPAKRVRAMACSFSSVPDWD
SDNHGWIDVLSASPADDNGGEGNAPEEFDVVAAADQIFGEAVGSIVVGVGSEQSVVVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAADDNSIRLPRKVGRTASSLPIRYAAPQLIHWPDDAAAVQLRICAHGRHIVLYVSWA
RCSMFREWLDTYWVCLDALAAAALLGGALDDTARALRRDARLAALWGALADRLCRRVL
VDVCARNGVTLEPTFMSLPDDVKAAILARLPDGDDLARAECTCAGLRRLVADRDEDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tränslation="MADTSPLHKIIGAAWWARPLIGRL/VILAHAAFLDAGFVSTGAA
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VVFYCVRRANDHJTYWICLOAPAAAALLAGGLDDTRALARRRGAKLAALMSLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PALHKIGYTDAVPDLPRWLSPEAKDFLRGCLQRRAGDRPTAAQLLQHPFISKSCGLNN
KETVKATWVSPTSALDATLWESESSSTDGEEVDDMSSNSPTGRIRAMACSCQTLPDWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NQEDEFISLSYCSERILLVAVHAADNNAASRKAGIKECSHDPRPSIPSRCAHNLFLSL
IFIQIDNSNVVPFAPKY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DRLCRRVIYDLCARNGYPVEPEHELMSLPDDVKVA I LARLAAGEDLARVECTCVGLNI
LVAEHDSTLWKPMYTKLRSQLRRRLARFLGVSYGEPTAVSWKARYVAVRRRRVPAAHDV
FMGEI LLPVMTEWMRVPWIRRYPPVPPPPFESPEEBETVVPRRRRRRAMPRDAGHGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AMPGGSKQPVLGGTPAFMAPEVARGEEQGLAADVWALGCTVIEMATGRAPWSDMDNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /trānslation="MAAAIIGVGGGGWTRLRSIGHGASGATVSLAADDASGELFVVKS
AGDAVAATARQQLRREWSVMSGLSSPHVLRCLGFVQAAAGAGGEHQLLLEYAPGGSLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARVVMPGGSKQPVLGGTPAFMAPBVARGEBQGPAADVWALGCTVIEMATGRAPWSDM
DDVLAALRMIGYTDAVPDLPPWLSPEAKDFLRRCMORRAGDRPTAAQLLQHPFVSKSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MAKPKTSPLHRVIGAARWDAERPLGRLLILAHAAFLDAGFVPAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IYAPLLDLDFDSFTRFWVFDDKPSPLPEEITVPRHRRRRRRRAMPRDAGHGLAARGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVVARNGDRLDESAFRAYAADVLRGLDYLHEKLVVHGDVKGSNVLVGADGRAKLADFG
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/db_xref="GI:31430012"
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/product="putative NPK1-related protein kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAPGHGGDKKQWRGAGAVHSPSSGFRWKHR"
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/note="unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /locus_tag="OSJNBb0072F04.12"
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              /locus tag="OSJNBb0072F04.10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /produčt="unknown protein"
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                                                                                                                                                                                                               rotein id="AAP51982.1"
o xref="GI:31430011"
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mRNA

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probabilty 1.000) with cleavage site probability 0.999 at
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probabilty_0.892) with cleavage site probability 0.890 at
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transl table=11
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complement (1253. .1660)
locus tag="NBD272"
function="COGS COG3293"
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complement(1853. .2488)
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                                         complement (887. .1698) /note="ISNE5"
    FRFFIHFALIVDHLISVNRP"
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2595. .3197
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locus tage="NE0270"

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OLVLDIGMIPVVPPKANRVSPWEYDVEMYKKRNEVERLFRRIKRFRRIFSRFDKLDSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chain, P., Lamerdin, J., Larimer, F., Regala, W., Land, M., Hauser, L., Hooper, A., Klotz, M., Norton, J., Sayavedra-Soto, L., Arciero, D., Hommes, N., Whittaker, M. and Arp, D.
Complete genome sequence of the ammonia-oxidizing bacterium and obligate chemolithoautokroph Nitrosomonas europaea
J. Bacteriol. 185 (9), 2759-2773 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313050 bp DNA linear BCT 23-APR-2 Nitrosomonas europaea ATCC 19718, complete genome; segment 2/10. BX321857, AL954747 BX321857,1 GI:30138174
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                                                                                                                                                                           Gaps
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                                                                                   3.4%; Score 21; DB 8; Length 303511;
100.0%; Pred. No. 2;
Live 0; Mismatches 0; Indels 0;
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complement (132. .503)
/locus_tag="NE0270"
complement (132. .503)
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Nitrosomonas europaea ATCC 19718
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complement (885, 1253)
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Location/Qualifiers
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Direct Submission
                                                                                                                             Best Local Similarity 100.
Matches 21; Conservative
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BX321857/c
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DEFINITION
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AUTHORS
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moleculaire, Universite Libre de Bruxelles, laboratoire de Biologie
du Developpement, Rue des chevaux, 67, 1640 Rhode St Genese,
BELGIUM
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                                                                                                                                          ROD 24-FEB-1999
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ESENVCQEDSDPDKFFABFIYEVSRRHPDLSTPRLLAITKYYMDFLEDCCSRENPÅG
CYRVJEDKFNETTQRSLAMVQGECNOFQELGKDTLQRHFLKRFTKAAPQLPMEELVSL
SKENVAALTTCCTLSDSFAVVDNLADLVLGELGGVNTNRTINPAVDHCKTDFRRH
CFEHLKADTTYALPSVSALVSALHTDMCQPRKEDLQNKKHRFLVNLVKWMPGITDEEW
                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (15-SEP-1998) Van Reeth T., departement de Biologie
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1. .2680
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                                                                                                                                          linear
                                                                                                                         2080 bp mRNA li
Mus musculus mRNA for alpha-albumin protein.
AJ011080
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alpha-albumin.
Mus musculus (house mouse)
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2 (bases 1 to 2080)
Van Reeth,T.
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                                                                                                RESULT 5
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AC117443/c
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HAIORLAEGAGYSVYREFCCHGIGAKFHBDPQVLHYGRAGTGIELKPGMIFTVEPMIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tränslation="mnkiviasnnagklabiskllaplgievvygsslgyteadephm
Tyvbnalakakhaklatoleplaladsosicvsklakoppowerernyksepreberdernkl
Verlatgosdrraytovivllahgoppopui iedywrebiiaepigogefgydphffi
Pelgktaaelsiebknrishrgkalarluomlsenetvpvvpv"
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LPLARGVEITUEANPGTLEAQKETDEHSAGINRLSIGTQSFRSRHLQALGKIHGAEA
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YRYPPQLPDEDTSAADMQVMIBHILABRGYRHYETSAPAQPGKFCLHNNNYWQYGDYLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IEKVPPFLKGAGGGWLTAEYGMLPRSTGERMQREAAKGKOSGRTMEIQRLIGRALRSI
LDLEKLGERTIQMDCDVIQADGGTRTASITGAFVALYDAIDYLRAERMISQNPIRDHV
AAVSVGILKGQPLLDLDYLEDSGCDTDLNVVWTGSLGLVEVQGTAEKVVFSRQELDVM
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MNALRLTEGFDPGLFHTRTGLTIASIQKSLAZAEQRGLIEWQHDCIRPTPEGRRFLND
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| locus tag="NB0278"

| function="InterPro IPR003401:IPR004559 COGs COG0635"

| codon start=1

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| transl table=1
                                                                                                                                                                                                                                                                                                                             function="InterPro IPR001247: IPR002381 COGs COG0689"
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Rukaryota; Merazas; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 2219)

1 (Dases 1 to 2219)

2 Murny, D. M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Albers, I. C., Eurel, S., Arej, R., Barks, T., Barbaria, J., Benchon, J., Branch, Barks, T., Barbaria, J., Benchon, J., Envert, C., Burrell, K.L., Bryank, M. P., Bunday, C., Burch, P., Burkett, C., Burrell, K.L., Bryank, M. P., Bunday, C., Burch, P., Burkett, C., Burrell, K.L., Brydi, M.C., Carcon, T. E., Carter, M., Cavazos, S.R., Chack, J., Chavez, D., Cord, C., Coyle, M.D., Dabhorne, S.R., David, R., Day, Carroll, L., Dederich, D. A., David, C.D., Cox, C., Coyle, M.D., Dabhorne, S.R., David, R., Day, Carroll, L., Dederich, D. A., Detaney, K.R., Dagar, D., Edwards, C.C., Elbaj, C., Escotto, M., Falls, T., Edyar, D., Edwards, C.C., Elbaj, C., Escotto, M., Falls, T., Edyar, D., Edwards, C.C., Elbaj, C., Escotto, M., Falls, T., Gorrell, G., Herrandez, O., Harris, K., Harrandez, O., Harris, K., Harris, K., Harrandez, O., Harris, K., Harris, C., Licu, Y., Licu, Y., Harris, K., Harris, K., Harris, K., Harris, C., Licu, Y., Harris, K., Har
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Submitted (26-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
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Submitted (10-APR-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
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(bases I to 22190)
   AC117443.4 GI:22024339
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3 (bases 1 to 22190)
Worley, K.C.
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Worley, K.C.
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                                                           Homo sapiens (human)
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                        ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 16:34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.hgsc.bcm.tmc.edu:8088/quallty.info/genbank.annotation.ht
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Exports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:
Baylor Plaza, Houston, TX 77030, USA on Jul 31, 2002 this sequence version replaced gi:20335979. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu
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586_ 5607
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/rpt_family="(TA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
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complement (2527, .25co)
/rpt_family
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2843. .2871
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/rpt_family="Af_rich"
3435, .3468
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/rpt_family="MER83-internal"
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/rpt_family="MER83-internal"
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complement(20204, .22100)
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complement(11511..11925)
/rpt_family="MLT1B"
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complement(13658..13691)
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rpt_family="THE18"
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ement(A010
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Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, P., DeArellano, K., Dewark, K., Dewark, R., Dodge, S., Paro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Baro, S., Dodge, S., Raco, B., Horton, L., Hulme, W., Tilev, D., Galagan, J., Gardyna, S. Gord, S., Craham, L., Grand-Pierre, N., Hafez, N., Halle, M., Tilev, T., Johnson, R., Jones, C., Indoblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldin, J., Macuer, L., Minova, T., Matthews, C., McCarthy, M., Meldin, J., Mayon, C., Nicol, R., Norbuc, Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vasaillev, H., Viel, R., Vo, A., Wilson, B. Wu, X., Direct Submission

Submitted (27-DEC-2002) Whitehead Institute/MIT Center for Genome All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
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100 bp
9 of 958 bp in length
100 bp
100 bp in length
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Mus musculus clone RP24-383E18, DNA linear HTG 27-DEC-2002 AC138385, GI:27375071
HTG; HTGS PHASE0.
Mus musculus (house mouse)
Bukarvor.
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Birren, B.; Nusbbaum, C. and Lander, E.
Mus musculus; clone RP24-383E18
Unpublished
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Birren, B., Musbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Backleau, C., Boun, T., Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cook, P., Cans, C., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, F., FitzGerald, M., Gage, D., Galagan, J., Gardyans, S., Gord, S., Graham, L., Gage, D., Galagan, J., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
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Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matchews, C., McCarthy, M., Meldrim, J., Meneus, L., Minova, T., Mlenga, V., Murphy, T., Maylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Connor, T., O'Connor, T., O'Neal, D., Olivez, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Scojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, N., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                              http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Web site: http://www.seq.wi.mit.edu
Contact: sequance submissions@genome.wi.mit.edu
Contact: project Information
Center project name: 1.26666
Center clone name: 383_E_18
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of 982 bp
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STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST
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I (bases I to 121201)

S Alams, Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Burbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bucck, J., Benton, J., Bireev, M., Brown, B., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carten, R., Chen, R., Daviel, M. L., Dederich, D., Daviel, N. L., Dederich, D., Delancy, K.R., Daviel, C., Davy-Carroll, L., Dederich, D., Daviel, M. L., Ding, Y., Harris, C., Harris, K., Harr
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Homo sapiens 3 BAC RPI1-535124 (Roswell Park Cancer Institute Human
BAC Library) complete sequence.
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Pred. No. 7.4;
B: contig of 1015 bp in length
B: gap of 100 bp
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0: contig of 999 bp in length
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7: contig of 999 bp in length
7: gap of 100 bp
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9: contig of 958 bp in length
1: gap of 100 bp
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4: contig of 959 bp in length
4: gap of 100 bp
9: contig of 997 bp in length
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llarity 100.0%; Pr
Conservative 0;
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Matches 20; Conserv
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Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S.,
Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J.,
Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C.,
Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W.,
Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Lurier, R.,
Martinez, E., Massey, E., Maunie, J., Martindale, A.,
Martinez, E., Massey, E., Maunie, S., Moreod, M. P., Meador, M.,
Moore, S., Morgan, M., Moorish, T., Morris, S., Moser, M., Nauyen, N.,
Nolson, D., Newtson, J., Newtson, N., Nguyen, N., Nguyen, N.,
Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N.,
Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N.,
Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N.,
Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Schers, S.,
Fickens, R., Primus, E., Pu, L.L., Quiles, M., Raves, M.,
Soct, G., Shen, H., Shooshtati, N., Sisson, I., Sodergren, E.,
Sonaike, T., Sparks, A., Stanley, H., Stone, H., Stutton, A., Svatek, A.,
Tabor, P., Tamerisa, A., Tamerisa, R., Wango, Y., Ward-Moore, S.,
Walliamson, A., Waleczyk, R., Wooden, S., Wulliams, G., Wu, Y.,
Wu, Y., Killiamson, A., Waleczyk, R., Naylor, S.L., Weinstock, G. and
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Direct Submission
Direct Submission
Submitted (25-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
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Submitted (26-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 121201)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (21-JUN-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, T77030, USA
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On Jun 21, 2003 this sequence version replaced gi:23307944.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 121201)
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Unpublished
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Direct Submission
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standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                         http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht
                                                                                                                                                                                                                                                      QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="overlaps bases 176428. .178521 of clone AC112644"
                                                                                                                  SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
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1659. .1180:
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/organism="Homo sapiens"
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complement(8672, 10086)
/rpt_family="L1PB1"
10087, 10516
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4169. .4349
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/db_xref="taxon:9606"
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complement(8280. .8524)
/rpt_family="L1PB1"
8525. .8671
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2802. .13984
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14730. .15081
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6406. .6462
/rpt_family="AT_rich"
complement(7193. .8279
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4756 4789
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5854. .5902
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4691_ 470
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complement(10517. .
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2308. .12600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome="3"
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Discrete B., Initon, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Birren, B., Initon, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barra, N., Baguslavkil, L., Boukhgalter, B., Brown, A., Camparate, J., Campoplano, A., Choepel, Y., Colangelo, M., Collins, S., Callymore, A., Cooke, P., Dehrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farc, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyete, M., Graham, L., Grand-Pierre, N., Gardan, L., Grand-Pierre, N., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, K., Liu, G., Machan, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McDena, T., Mlenga, V., Morbeters, R., Melthews, C., McCarthy, M., McDena, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norban, C., Norman, C.H., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Faback, M., Riley, R., Sougnez, C., Spencer, B., Stander, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stander, S., Schupback, R., Seaman, S., Tresfaye, S., Theodore, J., Travers, M., Trigillo, J., Young, G., Zainoun, J., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Wilson, B., and Zody, M., Young, G., Zainoun, J.,
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Homo sapiens chromosome 15 clone RP11-762M18 map 15, WORKING DRAFT SEQUENCE, 8 unordered pieces.
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HUGS PHASE; HTGS_FULLTOP.
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HOMO Sapiens (human)
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15971. .16501
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18720. .18761
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21358. 21407
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23313. .23405
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16514. 16799
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complement(16812. ,1
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Direct Submission

Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 15434)

Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barra,N., Bassiten,V., Bloom,T., Boguslawity,L., Boukhgalter,B., Canarata,J., Chang,J., Chararo,B., Chaepel,Y., Collymore,A., Canarata,J., Chang,J., Chang,J., Chang,J., Chang,J., Chang,J., Chang,J., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Farcy,B., FitzGerald,M., Gage,D., Adlagan,J., Gardham,L., Granda-Pierre,N., Hagos,B., Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Tch,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C., Norman,C., McCarthy,M., Meddim,J., Meneus,L., Micol,G., Madonald,P., Micol,R., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Roor,P., Smith,C., Spencer,B., Stanger-Thomann,N., Stojanovic,N., Talamas,J., Vola,K., Vola,M., Wilse,R., Samann,S., Severy,P., Smith,C., Spencer,B., Stanger-Thomann,N., Stojanovic,N., Talamas,J., Viel,R., Vola,M., Wilse,R., Naman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

Direct Submission

Submitted (66-Aug-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using Repeatmasker: Html

Center: Whitehead Institute/MIT Center for Genome Research

Center: Whitehead Institute/MIT Center for Genome Center

Center: Whitehead Institute/MIT Center for Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site, near the http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project name: 112158
Center clone name: 762 M.18
Center clone name: 762 M.18
Sequencing vector: Plasmid: n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 15220% bases at least Q30
Consensus quality: 15320% bases at least Q30
Consensus quality: 15340% bases at least Q20
Insert size: 157000; agarose-fp
Insert size: 154034; sum-of-contigs
Quality coverage: 8.6 in Q20 bases; sum-of-contigs
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Location/Qualifiers

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Stren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barra, N.; Bastien, V., Boguslavkiy, L., Boukhgaler, B., Brown, A., Camarata, J., Colamopalano, A., Choepel, Y., Colangolo, M., Collins, S., Collymore, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeArrellano, K., Dewar, K., Diaz, J.S., Gardynore, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Garada, S., Ginde, S., Goyette, M., Craham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Lilev, I., Johnson, R., Lehoczky, J., Levine, K., Liu, G., MacLean, C., Macdonald, P., Marquis, M., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Rieback, M., Riley, R., Rase, C., Rogov, P., Rosetti, M., Roy, A., Santos, R., Schuer, S., Schupback, R., Stange-Thomann, S., Schupack, S., Theodore, J., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
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Homo sapiens chromosome 15, clone RPI1-797A18, complete sequence.
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1 (bases 1 to 157793)

Birren, B., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 15, clone RP11-797A18
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100.0%; Pred. No. 7.8;
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                                                                                                                                                                       clone_lib="RPCI-11 Human Male BAC"
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5051. 5258
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                     /mol_type="genomic_DNJ/db_xref="taxon:9606"
/chromosome="15"
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/clone="RP11-762M18"
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Matches 20; Conservative
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JOURNAL REFERENCE AUTHORS

TITLE

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Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
           Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 17, 2003 this sequence version replaced gi:23308099. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                  Contact: sequence submissions@genome.wi.mit.edu
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complement(384. .433)
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complement (10024. .10310)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10002)
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/rpt_family="Aluy"
7645. .7983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="block".728)
/rpt_family="AluYc2"
459. ...69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (9074. . 9365)
                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: L12167
Center clone name: 797_A_18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9073)
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/rpt_family="AluJo"
2676. .2680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="RP11-797A18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="LiMA2"
2613. 2618
/note="<30 qual SNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (9681. .10
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complement(8869...9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'rpt family="AluSx"
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complement(8466..8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family="L1MB3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="L1MB3"
complement(9377...9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family="Alusg"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family="Alusg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="L1MB7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (10311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'rpt_family="Alu.
complement(9366.
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complement(10538
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1258<u>2</u>.
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12054.
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                                                                                                                                    Direct Summission

Submitted (17-FBB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, Musbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barrah, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cooke, P., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., Tizdersla, M., Gage, D., Galagan, J., Farce, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, T., Johnson, R., Dones, C., Kamat, A., Karates, A., Karlis, C., Landers, T., Levine, R., Lindblad, Toh, K., Liu, G., MacLean, C., Macdand, P., Major, J., Mathews, C., Norman, C.H., O'Connor, T., O'Donnell, P., Major, J., Mibova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicoll, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schuber, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Wo, A., Wilson, B., Wu, X., Waman, D., Young, G., Zainoun, J., Lamet, A., Milson, B., Wu, X., Waman, D., Young, G., Zainoun, J., Lamet, A., and Zody, M., Scholbor, A., Sainoun, J., Lamet, A., and Zody, M., Scholbor, A., Sainoun, J., Sewett, S., Savery, P., Sembek, L., Zimmer, A. and Zody, M., Scholbor, A., Waman, D., Young, G., Zainoun, J., Sewett, S., Savery, A., Scholbor, A., Waman, D., Young, G., Zainoun, J., Sambek, L., Zimmer, A., and Zody, M., Scholbor, A., Saviba, A., and Zody, M., Scholbor, A., Saviba, A., Saviba, A., Saviba, M., Saviba, M., Saviba, A., Saviba, 
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Research, 320 Charles Street, Cambridge, MA 02141, USA.

Research, 1co 157793)

Barna, N., Bastien, V., Bloom, T., Boguelavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Garnd-Pierre, N., Hafez, N., Hafez, N., Horton, L., Hulme, M., Illev, I., Johnson, R., Jones, C., Kamach, A., Kartas, A., Kartas, R., Kells, C., Landers, T., Levine, R., Macthews, C., McCarthy, M., Medlem, J., Meneus, L., Mihova, T., Matthews, C., McCarthy, M., Medlem, J., Meneus, L., Mihova, T., Murphy, T., Naylor, J., Nguyen, C., Micol, R., Norbu, C., Norman, C.H., O'Comnor, T., O'Domnoll, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Stanger, C., Regov, P., Roman, J., Roy, A., Schauer, S., Schubback, R., Stanger, Thavers, M., Y., Samman, S., Severy, P., Smith, C., Spencer, B., Stanger, Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Wyman, D., Young, G., Zainoun, J., Zambek, L., Zimmer, A. and Zody, M. Direct, Submission
Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
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Submitted (18-MAR-2003) Whitehead Institute/MIT Center for Genome
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TITLE JOURNAL

REFERENCE AUTHORS

TITLE JOURNAL

REFERENCE AUTHORS

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Research, 320 Charles Street, Cambridge, MA 02141, USA

Blirren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavkiy, L., Boukhgalter, B., Camarata, J., Chang, J., Chopel, Y.,
Collymore, A., Cook, A., Cooke, P., Corum, B., Dakrellano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreira, P., FitzGerald, M., Edge, D., Galagan, D., Hagos, B.,
Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kalls, C., Landers, T., Levine, R.,
Indublad-Toh, K., Liu, X., Lui, X., Mabbitt, R., Maclean, C.,
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Nell, D., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Nell, D., Oliver, J., Peterson, K., Phunkhang, P. Pierre, N.,
Radubka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Radubka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassillev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wann, D., Young, G., Zahnoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission

Submitted (15-DEC-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Dec 15, 2003 this sequence version replaced gi:38524692.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P.
Center, Whitehead Institute/ MIT Center for Genome Center for Genome Center center for Genome Center center for Genome Center center for Genome Center whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 1 2589: contig of 2589 bp in length.

* 2590 171061: contig of 100 bp

* Location/Qualifiers
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100.0%; Pred. No. 7.9;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: 1.20923
Center clone name: 176_C_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Matches 20, Conservative
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae, Murinae; Mus.
Burearyota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus chromosome 16, clone RP23-176C2
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B. Birren, B., Linton, L., Nusbaum, C., Changaro, Cooke, P., DeArellano, K., Dewar, K.; Diaz, J.S., Dodge, S., Faro, S., Foropel, Y., Colangelo, W., Callins, S., Collymore, A., Conarata, J., Camarata, J., Garad-Plarre, N., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Garddra, S., Gord, S., Marthew, T., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Landarares, R., Landers, T., Lehoczky, J., Lehoczky, J., Marquis, N., Matthews, C., McCarthy, M., Marquis, N., Matthews, C., McCarthy, M., Mayor, J., Marquis, N., Matthews, C., McCarthy, M., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Retta, R., Rieback, M., Riley, R., Rise, C., Rodyov, P., Roman, S., Severy, P., Spencer, B., Santos, R., Phuman, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Submission
Miscolar Submission
Miscolar Submission
Mannander Submission
Mannander Santos, R., Wallerd Institute (MI Center for Genome Submitted (03-FeB-cons)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus chromosome 16 clone RP23-176C2 map 16, *** SEQUENCING AC109266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.3%; Score 20; DB 9; Length 157793; Best Local Similarity 100.0%; Pred. No. 7.8; Matches 20; Conservative 0; Mismatches 0; Indels 0.
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Mus musculus (house mouse)
Mus musculus
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AC109266
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AUTHORS
TITLE
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ement (12770. .13056)
family="MER57-internal"
ement (13069. .13166)
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complement(21821. .21907)
/rpt family="Lip"
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ement(1277^
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/rpt_family="Alusp"
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complement(20647...
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:omplement(12770.
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Baxer, J. (Bases I to 1) **Obb No. |

Baxer, J. (Basel Le. |

Baxer, J. (Batladin, J. Barna, N. ) **Beckerly, R. ) **Benn, J. ' Boutwell, C. )

Baxer, J. (Batladin, J. ) **Depayre, B. ' Devon, K. )

Collymore, A. ' Cocke, P. ' Corliss, D. ' Depayre, B. ' Devon, K. )

Collymore, A. ' Cocke, P. ' Corliss, D. Depayre, B. ' Devon, K. '

Collymore, A. ' Gardyna, B. ' Garagery, K. ' Grant, G. ' Hadgos, B. ' Heaford, A. )

Gardyna, S. ' Garagery, K. ' Grant, G. ' Hadgos, B. ' Heaford, A. )

Herena, L. Horton, L. Howland, J. C. ' Jacctot, L. ' Jones, C. ' Kann, L. )

Karatas, A. ' Lehoczky, J. Macdonald, P. Marquis, N. ' McEwan, P. '

Mychaleckyj, J. Nahf, R. ' Madlan, J. ' Molla, M. ' Morrow, J. ' Mychaleckyj, J. ' Nahf, R. ' Nahla, J. ' Molla, M. ' O'Connor, T. '

Subramanian, A. ' Pavlin, B. ' Peterson, K. ' Riley, R. Roberts, D. ' Roy, A. '

Subramanian, A. ' Tesfaye, S. ' Tichvolsky, N. ' Torruella-Miler, I. '

Vassillev, H. ' Vo, A. ' Magner, A. ' Wheeler, J. ' Wu, Y. ' Wyman, D. ' Ve, W. J. ' Zhao, J. and Zody, M. '

Birect Submission

All repeats were identified using RepeatMasker: Smit, A. F. A. & Green, P. (1996-1997)

Hutp://ftp.genome.washington.edu/RM/RepeatMasker: Smit, A. F. A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                              Lander, B. Johnson, C. Lander, E. Allen, N., Anderson, M., Barren, B., Linton, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Barwa, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Donelan, L., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Harena, L., Horton, L., Howland, J. C., Jacotot, L., Jones, C., Kann, L., Karatas, A., Lehcozky, J., Maddonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychalecky, J., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Perrson, Y., Kiley, R., Roberts, D., Severy, P., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Ve, W. J., Zhao, J., and Marker, Wheeler, J., Wu, Y., Wyman, D., Ye, W. J., Zhao, J., and Cady, M., Torruella-Miller, I., Ye, W. J., Zhao, J., and Cady, M., Cannor, M., My Y., Wyman, D., Ye, W. J., Zhao, J., and Cady, M., Cannor, M., Cannor, M., Cannor, M., Cannor, C., Willer, M., Woller, C., Willer, M., Wyman, D., Ye, W. J., Zhao, J., and Cady, M., Cannor, C., Cannor, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens chromosome 17, clone hRPK.998 F.B, complete sequence.
                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 175066)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_'hRPK.998 F 8"
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                                                                                                     Homo sapiens (human)
Homo sapiens
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Mile Miles Miles (1900 MILE) Mile MILE (1900) MILE (19
            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (2008) 1 (2012) Birren, B., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research
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Mus musculus clone RP24-15911, WORKING DRAFT SEQUENCE, 6 ordered
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AC115834.4 GI:32567880
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.3%; Score 20; DB 9;
100.0%; Pred. No. 7.9;
ive 0; Mismatches
                                                                                          /rpL family="Tigger2"
complement(25255..25430)
/rpt family="MRRS0"
complement(25499..25627)
/rpt family="AluSg/x"
complement(15629..26179)
/rpt family="AluSg/x"
26205..26465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="LiPA5"
complement(35003. 35313)
/rpt_family="AluYa5"
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complement (29470.29778)
/rpt_family="AT_rich"
20002.30029
/rpt_family="AT_rich"
complement (31018.31069)
31070.31140
/rpt_family="LIMB3"
31070.31140
/rpt_family="(TA)n"
complement (31148.31164)
/rpt_family="(TA)n"
complement (31148.31164)
/rpt_family="Limb3"
/rpt_family="Limb3"
/rpt_family="Limb3"
                                                                                                                                                                                                                                                                                    /rpt_family="Trigger2"

complement (26829. 26851)

/rpt_family="purine-rich"

complement (26966. 27083)

/rpt_family="purine-rich"

27097. 27178.

/rpt_family="(CCGTT)n"

/rpt_family="(CCGTT)n"

/rpt_family="(CGGTT)n"

/rpt_family="(CGGTT)n"

/rpt_family="(GGGAA)n"

complement (27227. 27354)

/rpt_family="(GGGAA)n"

complement (27329. 27432)

/rpt_family="purine-rich"

complement (27820. 27432)

/rpt_family="purine-rich"

complement (27820. 27432)

/rpt_family="purine-rich"

complement (27820. 27432)

/rpt_family="purine-rich"

zensemplement (27850. 28932)
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/rpt family="Limbs"

complement (31788. 32098)

/rpt family="Aluy"

complement (32099. 32179)

/rpt family="Limbs"

complement (32099. 3462)

/rpt family="MERSA"

/rpt family="MERSA"

complement (33822. 33952)
/rpt_family="Tigger2"
24517. .24634
/rpt_family="Alusq/x"
24663. .25126
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complement(31463.
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Best Local Similarity 100.0
Matches 20, Conservative
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RESULT 14 AC115834 LOCUS DEFINITION

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ORGANISM ACCESSION VERSION KEYWORDS SOURCE

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regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (1.e., phred quality >= 0.0); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the cocasion of the clone being a YAC. This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 human chromosome 22, constructed by the Sanger Centre Chromosome 22 human chromosome 22 constructed by the Sanger Centre Chromosome 22 human chromosome 22 constructed by the Sanger Centre Chromosome 22 human chromosome 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RP5-1042X10 is from the library RPCI-5 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all
                                                                                                                 Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VECTOR: DCYPAC2
IMPORTANT: This sequence is not the entire insert of clone
RPS-104ZK10 It may be shorter because we sequence overlapping
sections only once, except for a short overlap.
The true left end of clone RPS-1042K10 is at 1 in this sequence.
The true left end of clone RP4-591N18 is at 184081 in this
sequence. The true right end of clone RP3-377F16 is at 39440 in
this sequence.
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Anote="Multip repeat: matches 140. .312 of consensus" complement(1419. .1459)
/note="MIR repeat: matches 32. .71 of consensus"
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/note="AluS repeat: matches 276. .298 of consensus"
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/note="AluY repeat: matches 1. .309 of consensus"
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   Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.sanger.ac.uk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DN
/db_xref="taxon:9606"
/chromosome="22"
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/clone_lib="RPCI-5"
1. .68
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                                 (bases 1 to 184180)
                                                                                     Direct Submission
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HUMBAN DNA SEQUENCE from Clone RP5-1042KIO on chromosome
22q13.1-13.2 Contains the ADSL gene for Adenylosuccinate lyase (EC
4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with
probable rabGAP domains and Src homology domain 3). Contains ESTS,
57GS, GSSs and a putative CpG island, complete sequence.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are represented as runs of N The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be preserved.

* This sequence will be preserved.

* This contign of 704 bp in length

* 1050

* 1450: contign of 646 bp in length

* 1551

* 105068: contign of 100 bp

* 105069: contign of 103518 bp in length

* 105069: li9607: contign of 1439 bp in length

* 119508

* 119608: 119607: gap of 100 bp

* 119608: 119607: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Consensus quality: 178697 bases at least Q30 Consensus quality: 179011 bases at least Q20 Insert size: 17660; agarose-fp Insert size: 179672; sum-of-contigs Quality coverage: 11.4 in Q20 bases; agarose-fp Quality coverage: 11.2 in Q20 bases; sum-of-contigs
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Pred. No. 7.9;
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3.3%; Score 20; ub.
Best Local Similarity 100.0%; Pred. No. 7.9
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/note="assembly_fragment"
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/note="assembly_fragment"
119608, .176231
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176332. .180172
/note="assembly_fragment
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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6143. ,7010
/note="Charlie2a repeat: matches 1445. ,2313 of consensus"
                                                                                                                                                                                                                                                                       copies 18 mer TCTCTTTCTCTTTC 51% conserved"
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                                                                                             repeat: matches 3242. .3313 of consensus"
         'note="AluSx repeat: matches 3. .287 of consensus"
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/note="#lusx repeat: matches 1. .287 of consensus"
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/note="Alux repeat: matches 1. .309 of consensus"
8856 . 8865
/note="2.0 copies 5 mer ATTTC 20% conserved"
                                                                                                                                                                                                                                                                                                                                    8123. .8144
//note="2.4 copies 9 mer TTTCGCTTT 35% conserved"
8127. .8147
/note="3.0 copies 7 mer TCTTTTT 24% conserved"
                                                                                                                                                                                                                                                                                                                 copies 8 mer TTCTTTCC 34% conserved"
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                                                                                                                                                                                 copies 6 mer CTTTCT 39% conserved"
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11602. .11616
/note="2.5 copies 6 mer GCCCCA 30% conserved"
/note="2.5 copies 6 mer GCCCCA 30% conserved"
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100.0%; Pred. No. 7.9;
ive 0; Mismatches 0; Indels 0
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                                                                                                 /wore="2.8 copies 4 mer CTTG 22% conserved" 8062. 8085 /note="4.0 copies 6
                                                                                                                                                                                                                                                                                                                                                                                                                          8137. .8151
/note="3.8 copies 4 mer CTTT 23% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8918. .8931
/note="3.5_copies 4 mer AAAT 28% conserved"
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/note="2.1 cc
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/note="3.3 cc
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/note="2.0 cc
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/note="4.5 co
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'note="3.3 c
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/note="12.
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/note="2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      evidence=not_experimental
product="dild42kl0.4" (novel protein)"
protein_id="CAA18263.1"
db_xref="GI:4176443"
(translation="RKISQAVRQQQEQQLARMVSALQQQQQQQQQQQQQQRHSPSHPVG")"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PKPHLDNMVDNALNVGLPDLQTYSGSPSGSPSSGSPSSGSSEGGTESTRYVY
SMMEGLPSYATQBANMHKNGAIVAPGKTRGGSPYNQPDIIPGGHTGBAGDSWLP
AKSPPTWKIGSKSSNASWPBFQPGYPWKGIQNIDPBSDPYTPGSYLGGHTGPAGDSWLP
TDHQLLRDNTTGSNSSLNAFWPPSPGYPWSSTAKFPDYKSTWDPDI
GHNPTHLSNYTAGSNSSLNTPPLPRPPYSASDNSFTNVHSTSAKFPDYKSTWDPDI
GHNPTHLSNYMWANTSRYTTPLPRPPYSASDNSFTNYHSTGSKSYRAFGYGODSKL
ASASTWSDGGSVRPSYWLVLHNLTPQIDGSTLRTICMQHGPLLTFHLNLTQGTALIRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .3318. .23457)
gene="40104210.4"
oin(<3190. .3233,3378. .3561,10740. .10877,13045. .13221,
4733. .14879,15130. .15225,17511. .17735,18170. .18240,
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Inote="11.0 copies 1 mer T 22% conserved"

Inote="3176

Inote="3 copies 3 mer GCA 35% conserved"

Inote="33,337,3378. .3561,10740. .10877,13045. .13221,

4733. .14879,15130. .15225,17511. .17735,18170. .18240,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="supported by GENSCAN and FGENES
natch: ESTs: Em:AA615306 Em:AA065323 Em:W80019 Em:N75651
Em:AA747718 Em:AA354286"
                                                                                                                                                                                                 note="LIME4a repeat: matches 5973. .6118 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |814. .3825
|note="6.0 copies 2 mer TG 24% conserved"
|complement(3826. .3970)
|note="LiMB4 repeat: matches 5746. .5893 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            581. .4879
note="AluSg repeat: matches 1. .299 of consensus"
986. .5106
note="Charlie2 repeat: matches 34. .149 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="MER46A repeat: matches 149. .167 of consensus"
                                                                 note="FLAM_C repeat: matches 1. .132 of consensus"
                         .299 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  999. .4074
note="MER46A repeat: matches 1. .82 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1401. .3425
/note="8.3 copies 3 mer GCA 50% conserved"
complement (3607. .3810)
/note="MIR_repeat: matches 19. .226 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="AluSx repeat: matches 1. .312 of consensus"
                                                                                                                                                       conserved"
                                                                                                                                                                                                                      648. .2666
note="3.8 copies 5 mer CTTT 31% conserved"
                                                                                                                                                                                                                                                              649. 2676

note=="28.0 copies 1 mer T 20% conserved"

650. -2665

note="4.0 copies 4 mer TTTC 23% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="5.3 copies 3 mer CTT 32% conserved" omplement (5266. .5553)
                                                                                                                             335. .2345
note="2.2 copies 5 mer TGTTT 22%
omplement(2420. .2548)
complement (1469. .1766)
/note="AluSp repeat: matches 1.
complement (1786. .1903)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  901. .4459
gene="dJ1042K10.4"
note="match: GSS: Em:AQ549653"
omplement(3974. .3998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        885. .4574
gene="dJ1042K10.4"
note="match: GSS: Em:AQ627708"
                                                                                      967. .2589 note="match: GSS: Em:B14103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="dJ1042K10.4"
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Abl26531 Drosophil
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Abx74808 Bacillus
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corynebacterium; gltBD; L-glutamic acid; PCR primer; ss.
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                                                                                                                                                                                                       Argaradaaarcaargaccrcaagaaarcrrrrggcgrrcggarcrrarggcaaggrcrc 1176
                                                                                                                                                                                                                                                   TCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATCCTTGTC 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                       1476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACAACAACT 1536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1597 GCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCGACAAA 1656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1657 GGCGCCACCGTTGTTGTTGCTACGCACTCGCCCCTCTTCCGAGAATCAGCGGATACCATT 1716
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                    The present invention describes a protein (1) which can be used to construct an ATP binding cassette (ABC) transporter. ABC transporter DNAs can be used in breeding Corynebacteria particularly for production of Lightennic acid. The present sequence encodes three ORFs (open reading
                                                                                                                                                                                                                                                                           180
                                                                                                                                                                                                                                                                                                                        GAGGATGTAGACCTTCTGAAACTCTCTACGCGTAAGCAACGGTTATACAGGAAAATACG 240
                                                                                                                                                                                                                               CTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACGAACT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCGCCACCGTTGTTGTTGCTACGCACTCGCCCTCTTCCGAGAATCAGCGGATACCATT 600
                                                                 frames) from the Brevibacterium lactofermentum gitBD gene, which is used in the exemplification of the present invention. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGCTTGCGGTGGAAAACACAAATGGCCTGAAATTCCTCAAGTACTTCATGCTGTTGGT
                                                                                                                                                                                  1 ATGATAGAAATCAATGACCTCAAGAAATCTTTTGGCGTTCGGATCTTATGGCAAGGTCTC
                                                                                                                                                                                                                                                                                                                                              GAGGATGTAGACCTTCTGAAACTCTCTACGCGTAAGCAACGGTTATACAGGAAAATACG
                                                                                                                                                                                                                                                                                                                                                                    GTGGGCTATTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAGTTAAATTTCAACCTT
                                                                                                                                                                                                                                                                                                                                                                                         GTGGGCTATTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAGTTAAATTCAACCTT
                                                                                                                                                                                                                                                                                                                                                                                                               CAGCTTGCGGTGGAAAAACACAAATGGCCTGAAATTCCTCAAGTACTTCATGCTGTTGGT
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                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brevibacterium lactofermentum gltBD gene PCR primer SEQ ID NO:6.
                                                                                                                                                            °
                                                                                                                                      Length 2370;
                                                                                                                Sequence 2370 BP; 633 A; 563 C; 515 G; 659 T; 0 U; 0 Other;
                                                                                                                                    tch 100.0%; Score 609; DB 3; Length 2 al Similarity 100.0%; Pred. No. 8.7e-310; 609; Conservative 0; Mismatches 0; Indels
Claim 14; Page 23-28; 34pp; Japanese.
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                                                                                                                                      Query Match
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The present invention describes a protein (1) which can be used to construct an ATP binding cassette (ABC) transporter. ABC transporter DNAs can be used in breeding Corynebacteria particularly for production of Inglutamic acid. The present sequence represents a PCR primer for the Exerbacterium lactofermentum gltBD gene, which is used in the exemplification of the present invention. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABC transporter constituent of Brevibacterium lactofermentum, its enco
gene and variants, applicable in breeding Corynebacteria particularly
production of L-glutamic acid.
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                                                                                                                                                                                                                                                                                                                                                                                            Nakamatsu T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 GCTCAACTGTCTTGGCACACTTGACAAACC 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ilarity 100.0%; Pred. No. 3.5
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 22; 34pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                            Kanno S, Kimura E, Matsui K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kimura E, Matsui K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA65393 standard; DNA; 22 BP
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Corynebacterium glutamicum.
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(first entry)
                                                                                                                                                                                                                                                                                                                            (AJIN ) AJINOMOTO CO INC.
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les 30; Conserv
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                                                            WO200037647-A1
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Gaps

antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that has an activity against a biological pathway computed for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound that inhibits the proliferation of an organism. The antisense mucleic acids required contifying proteins or screening for homologous mucleic acids required contifying proteins or screening for homologous mucleic acids required continual and account of a compound that inhibits the proliferation for screening for homologous mucleic acids required and account or a process of an organism. The antisense mucleic acids are useful for for callular proliferation of an organism. The antisense mucleic acids required and a proliferation of a compound that inhibits or actional and a second or and an organism of a conditional acids required and a second or an antisense mucleic acids required and a second or a condition of a cond

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Gaps ·;

drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. preumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the wipo.int/pub/published\_pct\_sequences

Gaps

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Mismatches

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Score 19; DB 7; Length 768; Pred. No. 20;

3.1%; Scc. 100.0%; Pre 0; '

Query Match Best Local Similarity 100. Matches 19, Conservative

Sequence 768 BP; 223 A; 149 C; 170 G; 226 T; 0 U; 0 Other;

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f Brevibacterium lactofermentum, its encoded in breeding Corynebacteria particularly for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                             The present invention describes a protein (I) which can be used to construct an APP binding cassette (ABC) transporter. ABC transporter can be used in breeding Corynebacteria particularly for production of glutamic acid. The present sequence represents a PCR primer for the Brevbacterium lactofermentum gltBD gene, which is used in the exemplification of the present invention. (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; ds; prokaryotic essential gene; cell proliferation;
drug design; gene.
                                                                                                                                                                                                             ch 3.6%; Score 22; DB 3; Length 22;
1 Similarity 100.0%; Pred. No. 0.56;
22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                       Sequence 22 BP; 5 A; 7 C; 5 G; 5 T; 0 U; 0 Other;
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Yamamoto R,
                                                    Disclosure; Page 21; 34pp; Japanese.
                                                                                                                                                                                                                                                                  165 CGGACAGATCCTTGTCGAGGAT 186
                                                                                                                                                                                                                                                                                  Prokaryotic essential gene #2684
    ABC transporter constituent of
gene and variants, applicable i
production of L-glutamic acid.
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
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08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acinetobacter baumannii.
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Trawick JD,
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  ABC transporter
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Wall D,
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New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
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                                                                                                                                                                                                                                                                                                                 DNA encoding Acinetobacter baumannii protein #340.
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                                 ADA29053 standard; DNA; 855
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P-PSDB; ADA33179.
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ADA2905.
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Zyskind JW; Xu HH;

Ohlsen KL, Forsyth RA,

SEQ ID NO 340; 328pp; English

Example;

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the

Claim 14; SEQ ID NO 8897; 1766pp; English.

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The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii nifection, and as biocontrol agents for plants. The present sequence represents DNA encoding an A. baumannii
                                                                                                                                                                                                                                                  protein.
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Sequence 855 BP; 239 A; 168 C; 193 G; 255 T; 0 U; 0 Other;

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0; Gaps
Score 19; DB 8; Length 855; Pred. No. 20;
                         0; Indels
          100.0%; Pred. No. 20, tive 0; Mismatches
                                                   115 GGAAAATCGACTTTGCTCA 133
                                                                               199 GGAAAATCGACTTTGCTCA 217
            Local Similarity 100.
 Query Match
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RESULT 6

Human; novel protein; ss; Antianaemic; osteopathic; antiinflammatory; findunomodullatory; oytostatic; neuroprotective; vulnerary; nootropic; antiaconvulsant; antiathritic; cerebroprotective; antifungal; antivities; antiallergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; Parkinson's disease; inflammacory disorder; cancer; asthma; osteoporosis; tissue regeneration; immune disorder. Human cDNA encoding a novel human protein #308.

Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage.

Claim 1; Page 706; 894pp; English.

The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for sequencing, for chromosome or gene mapping, in the production of recombinant proteins, and in generating anti-sense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise ASS2742/C

ID AAS22742/C

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AGS2742;

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AGS2742;

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AAS22742;

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Human cDNA encoding a novel human F

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Human novel protein; se; Antianaen

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Human; novel protein; antiallergic; dermat

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MO200155437-A2.

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C1an-2001; 2001W0-US002623.

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Tang YT, Liu C, Drmanac RT;

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Tolated polypeptides useful for t:

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The invention relates to polymeric

C1 their active domains. The polypept:

C2 their active domains. The polypeptides are

C3 markers, food supplements, and in

C1 caised against the polypeptides are

C2 markers, food supplements, and in

C2 captencing, for chromosome or gene

C3 carombinant proteins, and in generic

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C5 crombinant proteins, and in generic

C6 checomplant proteins, and in generic

C7 theory.

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levels, as tissue markers, and to isolate receptors or ligands. Polypeptides of the invention may also be useful in treating platelet disorders, stem cell disorders, regenerating bone, cartilage, tendon, ligament and/or nerve tissue, wound-healing, treating burns; promoting the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral solerosis, stroke, immune defloiencies resulting from bacterial, viral or fungal infection or from autoimmunity, cancer, allergy, asthma, graft-vergus-host disease, case, haemophilia, thrombosis, anti-inflammatory diseases, nervous system disorders, and infection. The present sequence encodes a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to polynucleotides encoding novel human proteins or their active domains. The polypeptides, polynucleotides and antibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant protein expression or activity. The polypeptides can be used as molecular weight markers, food supplements, and in antibody production. The polypeptides are used to identify compounds which bind to the polypeptides. Polynucleotides of the invention are used as probes and primers, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, novel protein, ss. Antianaemic, osteopathic, antiinflammatory, fimunomodulatory, cytostatic, neuroprotective; vulnerary, noctropic, anticonvulsant, antiarthritic, cerebroprotective, antifungal, antiarthritic, terebroprotective, antifungal, antivital, antibody, gene therapy, neurological dischmatic, thrombolytic, immunogen, antibody, gene therapy; neurological discrder; parkinson's disease; unflammatory disorder, cancer, asthma; osteoporosis; tissue regeneration; immune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                         3.0%; Score 18; DB 4; Length 446; 100.0%; Pred. No. 69; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                             Sequence 446 BP; 131 A; 90 C; 91 G; 134 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA encoding a novel human protein #72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 273-274; 894pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 AACACAAATGGCCTGAAA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS22506 standard; cDNA; 471 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    317 AACACAAATGGCCTGAAA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-JAN-2001; 2001WO-US002623.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT, Liu C, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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es 18; Conserv
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reading frame of the novel polynucleotide. The nucleic acid sequences

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recombinant proceins, and in generating anti-eense DNA or RNA and in gene recombinant proceins, and in generating anti-eense DNA or RNA and in gene therapy. Polypeptides of the invention can be used to target drugs to a tumour, in assays to determine biological activity, to raise antibodies/elicit an immune response, to determine quantitative protein levels, as tissue markers, and to isolate receptors or ligands.

Tolypeptides of the invention may also be useful in treating platelet disorders stem cell disorders, regenerating bone, cartilage, tendon, ilgament and/or nerve tissue, wound healing, treating burns, promoting the proliferation, differentiation and survival of stem cells, as a characeptive, treating osteoporosis and osteoarthritis, anaemia, albreimer's, parkinson's and Huntington's diseases, amylotrophic lateral clungal infection or from autoimmunity, cancer, allergy, asthma, graft-versues-host diseases, nervous system disorders, and infection. The present sequence encodes a protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH3631, whose sequence was determined by the technique of SBH (sequencing by hybridiation). Also included is a purified polypeptide comprising a sequence corresponding to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                     Sequence 471 BP; 135 A; 96 C; 98 G; 142 T; 0 U; 0 Other;
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ACH25483 standard; cDNA; 496 BP.
                                                                                                                                                                                                                                                                                                                                                      3.0%; Scc
Local Similarity 100.0%; Pi
es 18; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human adult ovary cDNA #3863
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JONES L W.
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(LABA/) 1
(STAC/) 4
(DICK/) 1
(JONE/)
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            are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies specific for it. The purified polypeptide is useful for generating antibodies specific for it. The present sequence for this patent did not form part of the printed specification, but was segdata.uspto.gov/sequence.html?DocID=20030073623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH5081, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tage (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, ss, sequencing by hybridisation, SBH, expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
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as hybridization probes, as oligomers for PCR, for chromosome and gene
mapping, in the recombinant production of protein, or in generating
antisense DNA or RNA.
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                                                                                                                                                                                                                                                                              Score 18; DB 8; Length 496; Pred. No. 69;
                                                                                                                                                                                                                                            Sequence 496 BP; 138 A; 92 C; 84 G; 165 T; 0 U; 17 Other;
                                                                                                                                                                                                                                                                                                               0; Indels
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                                                                                                                                                                                                                                                                                                                                                82 ACAATGACAGCACTGACT 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACH28170 standard; cDNA; 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human adult ovary cDNA #6550.
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                                                                                                                                                                                                                                                                            3.0%;
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                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 18; Conservative
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(STAC/)
(DICK/)
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ACH28170/c
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responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antibodies pecific for it. The present sequence is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP95124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosts and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus epidezmidis; open reading frame; ORF; bacterial infection; antibacterial; gene therapy; gene; ds.
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:2210.
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                                                                                                                                                                                                      Sequence 498 BP; 141 A; 96 C; 105 G; 143 T; 0 U; 13 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 621 BP; 234 A; 94 C; 102 G; 191 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                  0; Indels
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3.0%; Score 18; DB 8;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 18; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                          317 AACACAAATGGCCTGAAA 334
                                                                                                                                                                                                                                                                                                                                                                 AACACAAATGGCCTGAAA 193
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ABN92747
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL016175) and the encoded proteins (ABB57737-BPX2021). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                        Drosophila, developmental biology, cell signalling; insecticide;
                                                                                           Drosophila melanogaster genomic polynucleotide SEQ ID NO 31066.
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Pred. No. 68;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 31066; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1125 BP; 304 A; 251 C; 291 G; 279 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                Myers EW;
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100.0%; Pre-
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ABL26531 standard; DNA; 1125 BP
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                                                                                                                                                                                                                                                                                                                                                                                Li PWD,
                                                                                                                                                                                                                                                                      23-MAR-2001; 2001WO-US009231.
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11-JUL-2000; 2000US-00614150.
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                                                            (first entry)
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Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                          pharmaceutical; gene; ds.
                                                                                                                                                                       Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                  (PEKE ) PE CORP NY.
                                                                                                                                                                                                       WO200171042-A2
                                                            26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interactions
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Gaps

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27-SEP-2001

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The present invention describes an isolated or purified nucleic acid molecule (I) encoding a mammalian Gl polypeptide which modulates bone rescarption in osteoclast cells. (I) has osteopathic activity and can be used in gene therapy. Gl genes and polypeptides are useful for preventing or treating bone related diseases such as osteopetrosis or osteoporosis, and for proper osteoclast maturation and bone tissue resorption. Probes and antibodies raised against the Gl gene product can be used in phybridisation and immunological assays to screen for and detect the presence of either a normal or mutated gene or gene product. The present sequence encodes the mouse Gl osteoclast related protein, from the
             Gl; bone resorption; osteoclast; osteopathic; gene therapy; bone related disease; osteopetrosis; osteoporosis; osteoclast maturation; osteoclast related protein; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                     New Gl polypeptides and genes encoding them, useful for preventing or treating bone related diseases e.g. osteopetrosis or osteoporosis, and for modulating proper osteoclast maturation and bone tissue resorption.
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100.0%; Pred. No. 68;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2997 BP; 818 A; 642 C; 696 G; 841 T; 0 U; 0 Other;
                                                                                                                                           /*tag= a
/product= "osteoclast related protein GI"
                                                                                                                                                                                                                                                                                                                                                          Benachenou N;
                                                                                                        Location/Qualifiers
45. .1061
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                                                                                                                                                                                                                                                          25-SEP-2002; 2002WO-EP010721.
                                                                                                                                                                                                                                                                                          27-SEP-2001; 2001CA-02357987.
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Best Local Similarity 100.0
"...hes 18; Conservative
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                                                                                                                                                                                                                                                                                                                       (AVET ) AVENTIS PHARMA
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P-PSDB; ADA00896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention.
                                                                                                                                                                                            WO2003029283-A2
                                                                              Mus musculus,
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophilar. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA ABR32072). The sequence data for this parent did not form part of the princed specification, but was obtained in electronic form part of the from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                        New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3125 BP; 966 A; 597 C; 649 G; 913 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 31063; 21pp + Sequence Listing; English.
                                                                                                                                             Myers EW;
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                               23-MAR-2001; 2001WO-US009231.
                                                            23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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11-JUL-2000; 2000US-00614150.
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                                                                                                                                         Venter JC, Adams M,
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Drosophila melanogaster,

WO200171042-A2

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New oligonucleotide libraries comprising oligonucleotides which selectively hybridize to mRNAs transcribed from a transcription unit of a genome, useful for detecting tissue-, pathology-, and developmental-
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                                                                                                                                                                         WO200210449-A2
                                                                                                                                                                                                                                                   specific genes.
                                                                                                                                                                                 07-FEB-2002
                                                                                                                                                                                                                       Shoshan A,
                                                                                                                            ABN35170;
                                                                      Query Match
                                                                             Matches
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The invention relates to an isolated mucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences (ABL10511), expressed DNA sequences (ABL10511), expressed DNA sequences (ABL10811). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 18; DB 4; Length 11920;
Pred. No. 67;
Claim 1; SEQ ID NO 14557; 21pp + Sequence Listing; English.
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100.0%; Pre
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Matches 18; Conservative
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· 0 0; Indels Mismatches 2140 GAGGAAAGCCAGTTTT 2123 373 GAGGAAAAGCCAGTTTTT 390

ABN35170 standard; DNA; 60 BP.

(first entry) 15-JJL-2002

Human spliced transcript detection oligonucleotide SEQ ID NO:7918.

Human; mouse; rat; splice transcript; detection; RNA transcript; splice variant; transcriptome; oligonucleotide library; ss.

sapiens

28-JUL-2000; 2000US-0221607P. 02-MAY-2001; 2001US-0287724P.

(COMP-) COMPUGEN INC

Faigler S; Mintz L, Mintz E, Wasserman A, WPI; 2002-257383/30.

Example 1; SEQ ID NO 7918; 47pp; English

The present invention describes oligonuclectide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcribtom units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The oligonucleotide libraries are useful for detecting mRNAs from a biological sample, in expression profiling studies, in qualitatively or quantitatively characterising the corresponding transcriptome, and in

detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised mini libraries to detect transcriptome under a particular biological or pathological state, and so allowing the detection of tissue and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN2753 to ABNS9589 represent oligonucleotide sequences from tats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip. wipo.int/pub/published\_pot\_sequences ó Gaps .; 0 Length 60; Score 17; DB 6; Length 60; Pred. No. 2.4e+02; 0; Mismatches 0; Indels Sequence 60 BP; 16 A; 15 C; 15 G; 14 T; 0 U; 0 Other; Query Match 2.8%; Sc Best Local Similarity 100.0%; P Matches 17; Conservative 0; 373 GAGGAAAAGCCAGTTTT 389 59 GAGGAAAGCCAGTTT 43 \$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$\$ ò

Search completed: July 30, 2004, 15:35:53 Job time : 457 secs

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Query Match
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                                                                               July 30, 2004, 15:19:50 ; Search time 99 Seconds (without alignments) 3413.789 Million cell updates/sec
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1: /cgn2 6/ptodata/2/ina/5A COMB.seg:*
2: /cgn2 6/ptodata/2/ina/5B_COMB.seg:*
3: /cgn2 6/ptodata/2/ina/6A_COMB.seg:*
4: /cgn2 6/ptodata/2/ina/6B_COMB.seg:*
5: /cgn2 6/ptodata/2/ina/PCTUS COMB.seg:*
6: /cgn2_6/ptodata/2/ina/Packfiles1.seg:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-134-001C-2210
US-09-107-532A-6
US-08-718-904-109
US-09-449-249-109
US-09-107-532A-2667
US-09-107-532A-2667
US-09-107-532A-3337
US-09-620-312D-848
US-09-468-656A-5
US-09-468-656A-5
US-09-468-656A-5
US-09-468-656A-5
US-09-4132-994-58
US-09-312-283C-411
US-09-312-283C-412
US-09-312-283C-412
US-09-312-283C-311
                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                  682709 seqs, 277475446 residues
                                                                                                                                     US-09-868-338-7_COPY_1117_1725
609
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                                                                                                                                                                                                                                                                                                                                                            Post-processing: Listing first 45 summaries
                                                    nucleic search, using sw model
                                                                                                                                                                                         OLIGO_NUC
Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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RESULT 2
US-09-134-001C-2210
is sequence 2210, Application US/09134001C
is parent No. 6380370
is GENERAL INFORMATION:
is APPLICANT DOUGETE-Stamm et al
intila OF INVENTION: USUDIAND ANINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
intila OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
intila OF INVENTION: USUDIAND ANINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
intila OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
intila OF INVENTION NUMBER: US 60/064,964
intila OF INVENTION NUMBER: US 60/064,964
intila DATE: 1997-11-08
intila DATE: 1997-11-08
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WS-09-328-352-340

Sequence 340, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 340

LENGTH: 855
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48, Appl
1255, Ap
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1255, Ap
1259, Ap
1260, Ap
1260, Ap
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1260, Ap
127, Appl
13, Appl
13, Appl
13, Appl
14, Appl
14, Appl
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3.1%; Score 19; DB 4; Length 855;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 19; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Acinetobacter baumannii
US-09-328-352-340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.0%;
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Sequence 109. Application US/09449249
Sequence 109. Application US/09449249
Fatent No. 6503886
GENERAL INFORMATION:
Chandler, Lois Ann
Chandler, Lois Ann
Sosnowski, Barbara A.
TITLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAL
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
            GENERAL INFORMATION:
APPLICANT: Baird, J. Andrew
APPLICANT: Chandler, Lois Ann
APPLICANT: Chandler, Lois Ann
APPLICANT: Sosnowski, Barbara A.
TILLE OF INVENTION: COMPOSITIONS CONTAINING NUCLEIC ACIDS AND LIGANDS FOR THERAPE
NUMBER OF SEQUENCES: 128
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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COUNTRY: USA
ZIP: 98104-7092
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 24-No. 6503866-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.8%; Score 17; DB 3;
100.0%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTORNEY/AGENT INFORMATION:
NAME: No. 6037329tenburg Ph.D., Carol
NAME: No. 6037329tenburg Ph.D., Carol
REGIGGTRATION NUMBER: 39,317
REGIGGTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 760100.415C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-6031
INFORMATICN FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/718,904

FILING DATE: 24-SEP-1996

CLASSIFICATION: 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322 AAATGGCCTGAAATTCC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 AAATGGCCTGAAATTCC 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 700 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
                                                                                                                                                                                                                                CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                Sequence 6, Application US/09107532A
Sequence 6, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECTUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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2.8%; Score 17; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 17; Conservative 0; Mismatches 0; Indels
                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <UNKNOWN>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Artiniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 192 base pairs
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0
     Pred. No. 7.9;
                         Mismatches
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LOCATION: (B) LOCATION 1...192
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecium
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US-08-718-904-109
; Sequence 109, Application US/08718904
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: circular MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 192 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                         247 TATTTATTTCAAGATTAT 264
                                                                                                                     238 TATTTATTTCAAGATTAT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                466 GATGAACCAACCGGAGC 482
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                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachusetts
100.08;
  Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                               RESULT 3
US-09-107-532A-6/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-107-532A-6
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Sequence 2722, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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2.8%; Score 17; DB 4; Length 858;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                      Length 711;
                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.,
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <URKnown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR, APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arimiello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 4C-012
TELECOMMUNICATION INFORMATION:
TELEPRAM: (781) 893-8077
TELECOMMUNICATION INFORMATION:
TELEPRAM: (781) 893-8277
TELEPRAM: (781) 893-8277
TELEPRAM: 858 base paire
                                                                                                                                                                                                                                                                                      Query Match 2.8%; Score 17; DB 4;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches 0
                                                                      NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...711; SEQUENCE DESCRIPTION: SEQ ID NO: 2667: US-09-107-532A-2667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...858
SEQUENCE DESCRIPTION: SEQ ID NO: 2722:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
           ORIGINAL SOURCE: ORIGINAL SOURCE: ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPÓLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 858 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                           466 GATGAACCAACCGGAGC 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277 GATGAACCAACCGGAGC 293
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Patent No. 6583275
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/718,904
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INPORMATION:
NAMME: NO. 5503886tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
TELECOMMUNICATION INFORMATION:
TELESPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.8%; Score 17; DB 4;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 17; Conservative 0; Mismatches
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REDIGHT TYPE: CD/ROM ISO9660
COMPUTER: PC
COMP
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REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-807
INFORMATION FOR SEQ ID NO: 2667:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLGY: linear SEQ ID NO: 109: US-09-449-249-109
                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 700 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 711 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      322 AAATGGCCTGAAATTCC 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 7310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Dramac, Radoje T.
TITLE OF INVENTION: No. 656962el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784C1P2B
CURRENT APPLICATION NUMBER: US/09/620,312D
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
CONTUTER: PC
CORRATING SYSTEM: «Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/08151
ATTORNEY/AGRIT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 47-012
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
;
; SEQUENCE DESCRIPTION: (B) LOCATION 1...1497
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US-09-107-532A-3337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-620-312D-848/c
; Sequent No. 6569662
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3337:
SEQUENCE CHARACTERISTICS:
LENGTH: 1497 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 AAATCGACTTTGCTCAA 134
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Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
Wang, Dunrui
Wang, Zhiwei
John Tillinghast
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Ren, Felyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
Xue, Aidong J.
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Liu, Chenghua
Asundi, Vinod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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Sequence 3337, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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2.8%; Score 17; DB 2; Length 1127;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                 RESULT B
US-07-35-068-1
| Sequence 1, Application US/07735068
| Patent No. 5885769
| Patent No. 58857696|
| GENERAL INFORMATION:
| APPLICANT: Kumar, Chanakanti C. TITLE OF INVENTION: No. 58857696| Screening Systems NUMBER OF SQUENCES: 4 NUMBER OF SQUENCES: 4 NUMBER OF SQUENCES: 4 NUMBER OF SGUENCES: 4 STREE: One Giralda Farms | STREE: New Jersey | STREE: New Jersey | COUNTRY: USA | COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THEAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTE. New CLILL
COUNTRY.

ZIP: 07940-100
COMPUTER READABLE
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 4.00B
SOFTWARE: Microsoft Word 4.00B
SOFTWARE: 19910724
CLASSIFICATION UMBER: US/07/735,068
FILING DATE: 19910724
APPLICATION NUMBER: US/07/735,068
FILING DATE: 19910724
APPLICATION NUMBER: US/07/735,068
FILING DATE: 19910724
APPLICATION NUMBER: US/07/735,068
FILING DATE: 19910734
ATTORNEY/AGENT INFORMATION:
NAME: DULAK, NO. 5885769man C.
REGISTRATION NUMBER: 1D0178K
TELECAMONICATION INFORMATION:
TELEFAX: 20182 7375
TELEX: 20182 7375
TELECAMONICATION INFORMATION:
TELECA
                                                        109 GGTTCAGGAAAATCGAC 125
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                                                                                                                                       145 GGTTCAGGAAAATCGAC 161
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STATE: Massachusetts
COUNTRY: USA
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US-07-735-068-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-09-107-532A-3337
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TYPE: nucleic acid
STRANDEDNESS: double
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US-08-961-527-94
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Sequence 5, Application US/09468656A

GENERAL INPORMATION:

APPLICANT: Johnson, Leslie S.

APPLICANT: Adamou, John E.

TITLE OF INVENTION: Wordine Group A and B Having Selected Structural

TITLE OF INVENTION: Motifs

FILE REPRESENCE: 46920.1444

CURRENT APPLICATION NUMBER: 05/113,048

PRIOR APPLICATION NUMBER: 60/113,048

NUMBER OF SEQ ID NOS: 14

SOFTWARE: Patentin Ver. 2.1
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Patent No. 6376210
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REPREBENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347,878C

CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75

SOFTWARE: Patentin Ver. 2.0
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100.0%; Pred. No. 28;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          2.8%; Score 17; DB 100.0%; Pred. No. 28; tive 0; Mismatches
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 848
LENGTH: 2351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-09-468-656A-5
                                                                                                                                                                                                                                                                                                                      COCATION: (1).T.(2351)
COTHER INFORMATION: n = a,t,c or g
US-09-620-312D-848
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Best Local Similarity 100.0
Matches 17, Conservative
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc feature
                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (46)..(1422)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-09-468-656A-5
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LENGTH: 2531
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US-09-347-878-25
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Sequence 94, Application US/08961527
Patent No. 6420135
Patent No. 6420136
PAPPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                       0
| SEQ ID NO 25
| LENGTH: 2561
| TYPE: DNA
| ORGANISM: Bscherichia coli
| PEATURE:
| NAME/KEY: CDS
| LOCATION: (1131)..(2399)
| OTHER INFORMATION: Escherichia coli nucleic acid encoding
| OTHER INFORMATION: Folypolyglutamate synthetase-dihydrofolate
| OTHER INFORMATION: SYNTHETASE
| PUBLICATION INFORMATION: SYNTHETASE
| PUBLICATION INFORMATION: NUMBER: M32445/GenBank
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                                                                                                                                                                                                                                                                                                                                    DB 4; Length 2561; 28;
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Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER FABDABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectre 486/33
OPERATING SYSTEM: MSDGS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                               Query Match
2.8%; Score 17; DB
Best Local Similarity 100.0%; Pred. No. 28;
Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: GALOKESS:
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Brockes, A. Anders
REGIETRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1116 GAATCAGCGGATACCAT 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.8%; Sci
Best Local Similarity 100.0%; P.
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                         583 GAATCAGCGGATACCAT 599
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ATTORNEY/AGENT INFORMATION:
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Sequence 1676, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT PELING DATE: 1998-08-13

PRIOR FILING DATE: 1999-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 1676

LENGTH: 183
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Patent No. 6228643
GENERAL INFORMATION:
APPLICANT: Thomas, Didler RP
APPLICANT: Thomas, Didler RP
APPLICANT: Thomas, Didler RP
APPLICANT: Thomas, Didler RP
APPLICANT: Depson, Ian
CURRENT APPLICATION NUMBER: US/08/821,994A
CURRENT APPLICATION NUMBER: DCT/GB97/00729
EARLIER APPLICATION NUMBER: DCT/GB97/00729
EARLIER APPLICATION NUMBER: GB 9606062.9
EARLIER PILING DATE: 1997-03-18
EARLIER PILING DATE: 1996-03-22
NUMBER OF SEQ ID NOS: 89
SOFTWARE: PATENTIN OF SEQ ID NOS: 89
SOFTWARE: PATENTIN OF SEQ ID NOS: 89
CONTWARE: BATENTIN OF SEQ ID NOS: 80
CONTWARE: BATENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
CCATION: 136, 187, 192
CTHER INFORMATION: n is unknown
US-08-821-994-58
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US-08-821-994-58/c
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RESULT 14
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Search completed: July 30, 2004, 17:25:10 Job time : 100 secs

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RESULT 1
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AV279945 AV279945	AV283498 AV283498	BB522412 BB522412	AW319130 un03£03.x
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COMMENT

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0 AW2105 AIS7387 AI87467 AW01256 AI31734 AA39704	ALLICES	A1196816 A1042942 A1042942 A1046692 A1346692 A1046692 A1046692 A1046692 A1046692 A1046692 A104692	744608478877
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V279945/c	
SOCOS	AV279945 231 bp mRNA linear EST 05-NOV-1999
EFINITION	AV279945 RIXEN full-length enriched, adult male testis (DH10B) Mus
	musculus cDNA clone 4933411H02 3' similar to AJ011080 Mus musculus
	mRNA for alpha-albumin protein, mRNA sequence.
CCESSION	AV279945
FRSION	AV279945.1 GI:6267982
CEYWORDS	BST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
	Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
RFERENCE	1 (bases 1 to 231)
AUTHORS	Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
	Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
	Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kaqawa, I.,
	Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,
	Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
	Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K.,
	Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y.,
	Suzuki, H., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N.,
	Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A.,
	Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
TITLE	RIKEN Mouse ESTs (Konno, H., et al. 1999)
JOURNAL	Unpublished (1999)
OMMENT	Contact: Yoshihide Hayashizaki

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Konno, H. Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Sahi, Y., Kaya, S., Kadaka, I., Kadota, Y., Kadawa, I., Kai, C., Kawa, T., Kiran, Y., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Shibata, X., Saito, H., Sano, M., Sato, K., Shibata, X., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Suzuki, H., Takahashi, F., Tateno, M., Tominaga, N., Tominada, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yookia, T., Yoshino, M., Muramatsu, M., and Hayashizaki, Y. Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   properated and sequenced in Mouse Genome Encyclopedia propared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was GAGAGAGAGAGAGAGCTCTTTTTTTTTTVN 3'), cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Yoshihide Hayashizaki
Laboratoryy for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Vokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-503-922
Fax: 81-45-503-9226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh.M. Kitsunai. T., Akiyama. J., Shibata, K., Izawa. M., Kawai. J., Tomaru. Y., Carninci. P., Shibata, Y., Ozawa, Y., Muramatsu. M., Cawai. Y., Akzaki, Y. and Hayashizaki, Y. And Hayashizaki, Y. And Hayashizaki, Y. Shibata, G. S. Asia, C. S. Shibata, S. S
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                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 244)
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URL:http://genome.gc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Fayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
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32;
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/dev_stage="adult"
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/strain="C57BL/6J"
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        ORGANISM
                                                                                                                        REFERENCE
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AV283498 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4933435E11 3' similar to AJ011080 Mus musculus mNNA for alpha-albumin protein, mNNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                      Transcriptional sequencing: A method for DNA sequencing using RNA polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998) Itoh, M., Kitsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J., Chazut, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Graninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
17-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="RIKEN full-length enriched, adult male testis (DR10B)"
                                                                                                                                                                                                                                            Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Ssaski,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4933411H02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="testis"
/dev_stage="adult"
/lab_host="DH108"
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EST.
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                                                                                                                                                            Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AV283498/c
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The Manualai and Determination of the Martin, The Martingery Full of Marra, M. Hillier L., Kucaba, T., Martin, G., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Thaising B., Allen, M., Bowers, T., Underwood, K., Swaller, T., Gibons, M., Pape, D., Harvey, M., Schurk, R., Watter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Watterston, R. and Wilson, R.

The Washb-NCI Mouse EST Project 1999
Unpublished (1999)
Other_ESTS = 1001603.y1
Contact: Marra M/Mashb-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW319130 353 bp mRNA linear EST 25-JAN-2000 un03f03.x1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2372765 3' similar to SW:AFAM_MOUSE 089020 AFAMIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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/lab_host="DH10B"
/clone_lib="Sugano mouse kidney mkia"
/clone_lib="Sugano mouse kidney mkia"
/clone_lib="Sugano mouse kidney wellow mkia"
/note="Organ: kidney; Vector: pME18S-FL3; Site 1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels 0; Gaps
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Location/Qualifiers
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/strain="C57BL"
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 303)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,

Araninci, P., Endo, T., Fukuda, S., Hakunishi, Y., Hara, A., Hayatsu, N.,

Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,

Kiyosawa, M., Kadgawa, T., Kai, C., Kawai, J., Kikuchi, N.,

Kiyosawa, H., Kojima, Y., Kando, S., Koya, S., Kurihara, C.,

Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M.,

Kiyosawa, M., Sujana, Y., Sujana, M., Sakai, C., Sato, K.,

Shibata, K., Shibata, Y., Sujanki, H., Suzuki, H., Tagawa, A., Shiraki, T.,

Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Wathhiki, A.,

Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and

Hayashizaki, Y.,

Takahashizaki, Y.,

Takahash
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-922
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Fax: 81-45-503-9216
Fax: 81-45-503-9216
Fax: 81-45-503-9216
Fax: 81-45-503-9216
Fax: 81-45-503-922
Fax: 81-45-503-922
Fax: 81-45-503-922
Fax: 81-45-503-922
Fax: 81-45-503-926
Fax: 81-45-903-92
Fax: 81-
                                                                                                                                                                                                                                                                                                                                                                                         BB522412 RIKEN full-length enriched, 15 days embryo head Mus musculus CDNA clone D930007074 3' similar to AJ011080 Mus musculus charalpha-albumin protein, mRNA sequence.
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                  0; Gaps
                      0; Indels
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/dev_stage="15 days embryo"
/lab_host="DH10B"
                  0; Mismatches
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Unpublished (2000)
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/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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BB522412.1 GI:9573870
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                  20; Conservative
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19-44 (1999)
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BB522412/c
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COMMENT
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AUTHORS
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3.3%; Score 20; DB 9; Length 368;
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JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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SOURCE
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/lab_host="DHIOB"
/lab_host="DHIOB"
/lab_host="DHIOB"
/lab_host="DHIOB"
/lab_host="United by the part of the
was primed with an oligo(dT) primer [ATGTGGCCTTTTTTTTTTTT]; double-stranded cDNA was ligated to a Drall adaptor [GGTGGGCTACTGG], digested and cloned into distinct Drall sites of the pWE183-FL3 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the CDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 03-DEC-1999
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Moderwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbon, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., The WashU-Nor Mouse EST Project 1999

Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AWAINDEL BST 03-DEC-199, UM62all.xl Sugano mouse kidney mkia Mus musculus cDNA clone INAGE:2285948 3' similar to SW:AFAM_MOUSE 089020 AFAMIN PRECURSOR AND ABAMIN A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contract: Marra M/MashU-NCI Mouse EST Project 1999
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.3%; Score 20; DB 10; Length 353;
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fsrain="C5'BL"

/db_xref="taxon:10090"

/clone="IMAGE:2285948"

/sex="female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: custom primer used. Location/Qualifiers
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       382 CCAGTTTTGAACTCT
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AW210581
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VERSION

SOURCE

ORIGIN

8 g COMMENT

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/done_libe_Ngaro mouse kidney mkia"
/dlone_libe_Ngaro mouse kidney mkia"
/note="Organ: kidney; Vector: pmb185-Fi1; Site_1: DraIII
(CACTGTGTG): Site_2: DraIII (CACCATGTG); 1st Strand CDNA
was primed with an oligo(dT) prime.
[ARGTGGCCTTTTTTTTTTTTTT]: double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pM2185-FI1
vector (5' site CACTGTGTG, 3' site CACCATGTG). Xno! should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCACACA."
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constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGGTCTAAAGGTGGG and 3' end primer CGACCTGCAGACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI573872 368 bp mRNA linear EST 29-MAR-1999
uj17d06.x1 Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:1908299 3' similar to SW:AFAM_RAT P36953 AFAMIN PRECURSOR ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Butheria; Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 368)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Marra, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R., The Washu-NcI Mouse BST Project 1999
Unpublished (1999)
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                                                                                                                                                                                                                                                                            Gaps
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
1811 314 256 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
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                                                                                                                                                                                                       3.3%; Score 20; DB 10; Length 362; 00.0%; Pred. No. 33;
                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                           Similarity 100.0%; Pred. wc. --. Similarity 0, Mismatches
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/clone="IMAGE:1908299"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                 382 CCAGTTTTGAACTCTCTGG 401
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Mus musculus
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/strain="C57BL"
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Matches

ò g LOCUS DEFINITION

A1874676 RESULT 7

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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183 bp mRNA linear EST 10-SEP-1999 ul69al0.x1 Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2135802 3' similar to TR:089020 089020 ALPHA-ALBUMINE PROTEIN, ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST 17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 33).
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TEL: 314 286 1800
Fax: 314 286 1810
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100.0%; Pred. No. 33;
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Contact: Marra M/WashU-NCI Mouse EST Project 1999
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/mol_type="mRNA"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
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/clone="IMAGE:2135802"
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Location/Qualifiers
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/lab_host="DH10B"
                                       CCAGTTTTTGAACTCTCTGG 205
                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL , contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
FTE1: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                               AI874676
379 bp mRNA linear EST 21-:
ul25a10.Xl Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:2099322 3' similar to TR:089020 089020 ALPHA-ALBUMINB
PROTEIN, ;, mRNA sequence.
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                                                                0; Indels
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                                 Pred. No. 33; Mismatches
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High quality sequence stop: 368.
Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:2099322"
                                                                                                              382 CCAGTTTTTGAACTCTCTGG 401
                                                                                                                                                      174 CCAGTTTTTGAACTCTCTGG 193
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Mus musculus
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                                                          20; Conservative
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Query Match
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Matches 20; Conserv
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AA260497/c
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/dev stage="adult"
/lab_host="DH10B"
/clone lib="Sugano mouse kidney mkia"
/clone lib="Sugano mouse kidney mkia"
/clone lib="Sugano mouse kidney mkia"
/note="Organ: kidney; Vector: pME188-FL3; Site l: DraIII
(CACTGTGTO); Site 2: DraIII (CACCATGTG); lst sTrand cDNA
was primed with an oligo(dT) primer
[ATGTGGCTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pME188-FL3
vector (s' site CACTGTGTG, 3' site CACATGTGG). KhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGTTCTAAAAGCTGCG and 3' end
primer CGACCTGCAAGCACA."
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                                                                                                                                                       uj13e04.xl Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:1907934 3' similar to SW:AFAM_RAT P36953 AFAMIN PRECURSOR ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:976130
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Unpublished (1996)
Contact: Marza M/Mouse EST Project
WashU-HHMI Wouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1810
Email: mouseest@watson.wustl.edu
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100.0%; Pred. No. 33;
iive 0; Mismatches 0; Indels
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/organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL"
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/clone="IMAGE:1907934"
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EST.
Mus musculus (house mouse)
                                                                                                                          Mus musculus (house mouse)
                                                                                   AI317342.1 GI:4032609
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                                                 MRNA sequence.
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AA397040/c
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AAZ60497 427 bp mRNA linear EST 18-MAR-1997 va95g10.r1 Soares mouse NML Mus musculus CDNA clone IMAGE:747234 5' similar to SW:AFAM_RAT P36953 AFAMIN PRECURSOR ;, mRNA sequence. AAZ60497
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1 (bases 1 to 427)

2 (barra,M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 417)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gachelle,X., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Chordata, Craniata, Vertebrata, Buteleostomi, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                               Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
Fax: 314 286 1810
Fax: mousesstowatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
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ive 0; Mismatches
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
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The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
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Location/Qualifiers
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Gaps

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Length 440; Indels

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Unpublished (2001)
Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Contactory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-2 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-2 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-2 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-13 1-3-503-9216
Email: genome-reseger.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
URL:http://gen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BB690607 BIKEN full-length enriched, 12 days embryo female mullerian duct Mus musculus cDNA clone 6820448P03 3', mRNA
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                               /clone_lib="pBluescript Lion"
                                                                                                                                                                                                                                                                                     3.3%; Score 20; DB 1
100.0%; Pred. No. 33;
ive 0; Mismatches
1. .440
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                                                             /mol_type="mRNA"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                           Local Similarity 100. es 20; Conservative
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DEFINITION
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BB690607/c
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BX635140 pBluescript Lion Mus musculus cDNA clone LIOND462D02381
3', mRNA sequence.
BX635140. GI:33615015
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Henrich, J., Herman, J., Kranz, H., Loebbert, R., Schlueter, T., Schuette, D., Weindel, M., Heil, O., Ebert, L., Neubert, P., Peters, M., Radelof, U., Schneider, D. and Korn, B.
Unpublished (2003)
Contact: Ina Rolfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: RP: CAGGAAACAGCTATGAC.
                                                             Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This Clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:456218
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Im Neuenheimer Peld 580, D-69120 Heidelberg, Germany
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             Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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100.0%; Pred. No. 33;
ive 0; Mismatches 0; Indels
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                           High quality sequence stop: 406.
Location/Qualifiers
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RZPDLIB;
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Matches 20; Conserv
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1. .455
/organism="Mus musculus"
      High quality sequence stop: 358.
Location/Qualifiers
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BB747871/c
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Matches
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus.
1 (Dases 1 to 455)
S Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood, K., Steptoce,M., Theising,B., Allen,M., Bowers,Y.,
Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R.,
Riter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Materston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
On Peb 10, 1999 this sequence version replaced gi:4060832.
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                               455 bp mRNA linear EST 07-MAR-2000 clone IMAGE:522099 3' similar to SW:AFAM_RAT P36953 AFAMIN A1427599 ; mRNA sequence.
                                                                                                                                                                                                                                                              /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was GAGAGAGAAGGTCCAAGAGCTCTTTTTTTTTTTTTTVN 3''), cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                              'tissue_type="mullerian duct includes surrounding region"
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Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                Gaps
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/clone="6820448P03"
    Location/Qualifiers
                                                          /mol_type="mRNA"
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                                                                                                                                               /sex="female"
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Contact: Yoshinide Hayashizaki
Contact: Yoshinide Hayashizaki
Contact: Yoshinide Hayashizaki
Contactror for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Sushirto-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-22 Sushirto-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-22 Sushirto-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-23 Sushirto-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-23 Sushirto-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-7-23 Sushirto-cho, Tsurumi-ku, Yokohama, Ku, Yokohama, Ku, Yohibata, Y.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M., Johara,E.,
Watahiki,M., Yoheda,Y., Ishibaries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Pujuwake,S., Inoue,K., Togawa,X., Tzawa,M., Ohara,E.,
Watahiki,M., Yoheda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
PITRN incorreted
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**Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T., Hayatesu,N., Hiramcho,K., Hiracaka,T., Hiracaha,T., Inoctani,K., Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Okazaki,Y., Okazaki,Y., Satio,R., Nomura,K., Numasaki,R., Okazaki,Y., Satio,R., Sakai,C., Sakazi,K., Sakazime,N., Sasaki,D., Sato,K., Shibata,K., Takaki,Y., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A., Muramatsu,M. and Hayashiaski,Y.
**RIKEN Encyclopedia of Mouse Full-length cDNAS (Akimura,T., et al.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res..
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Ouery Match
3.3%; Score 20; DB 10; Length 463;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 20; Conservative 0; Mismatches 0; Indels 0;

Qy 382 CCAGTTTTGAACTCTCGG 401

ORIGIN

Gaps

Search completed: July 30, 2004, 17:23:28 Job time : 2797 secs

284 ccadririrgaacrcrcdg 265

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GenCore version 5.1.6
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July 30, 2004, 07:14:14 ; Search time 3631 Seconds (without alignments) 7269.597 Million cell updates/sec US-09-868-338-7\_COPY\_1117\_1725 609 1 atgatagaaatcaatgacct.......cggataccattatcaaacta 609 6940544 Total number of hits satisfying chosen parameters: 3470272 segs, 21671516995 residues Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries OM nucleic - nucleic search, using sw model IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Minimum DB seq length: 0 Maximum DB seq length: 200000000 GenEmbl:\*

1: 9D ba:\*

3: 9D htg:\*

3: 9D on:\*

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9D pat:\* em om: \*
em or: \* Title: Perfect score: Scoring table: Database : Sequence: Searched: Run on:

21: em\_or:\*
22: em\_or:\*
23: em\_or:\*
24: em\_ph:\*
25: em\_ph:\*
26: em\_ro:\*
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27: em\_sts:\*
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39: em\_htg\_htm::\*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.   Score   Match Length DB   ID	## Score Match Length DB ID    10	## Built						SUMMARIES	
1 96.4 15.8 11364 1 AE010640 2 91.8 13.41553 1 BX248355 3 84.6 13.3 347961 1 BXS71557 AP003515 4 83.6 13.7 301439 1 AE0105943 AB0015943 8 83.6 13.7 301439 1 AE015943 AB0015943 8 82 13.5 10415 1 AE000977 AB0019315 8 82 13.5 10415 1 AE000977 AB0019318 8 82 13.5 10415 1 AE000977 AB0019318 8 80.8 13.3 349380 6 AX417049 AX417049 10 80.8 13.3 349380 6 AX417049 AX417049 11 80.6 13.2 1349380 6 AX417049 AX413018 12 108.1 10.2 11851 1 AE004555 AB016455 12 10.8 13.1 349380 6 AX417049 AX413018 13 10.2 1252 10.8 1 AE00455 AB016455 14 12.4 10.6 1 AE00465 AB006428 15 10.8 13.1 31160 1 AE00465 AB006428 16 17.4 12.4 10.0 1 AE00465 AB006428 17.4 12.4 10.0 6 AX51010 AB00716 AB007376 17.5 1 12.3 301289 AX41669 AX51166 17.5 1 12.3 301289 AX51010 AB007376 17.6 12.2 12.2 12.2 12.2 12.2 12.2 12.2 12	15.8   11564   1   1   1   1   1   1   1   1   1	15.8   11964   18X246355   1	Sul	Ö	% Query Match	Len	DB	ΠD	escripti
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3         84.6         13.9         347961         1 BX571657         BX571657         BX571657           4         83.6         13.9         54310         1 BX571657         AB015945           6         83.6         13.7         301339         1 AB015945         AB015945           8         13.6         13.1         30415         1 AB015943         AB015945           9         8         13.5         10415         1 AB015943         AB015943           9         8         13.5         10415         1 AB015943         AB01749           10         8         13.3         342980         6 AX417049         AX417049           11         10         13.2         1941         AX417049         AX417049           12         13.1         10739         AX417049         AX417049           13         13.1         10739         AX417049         AX417049	13.6 13.9 347961 1 BX551657 ABC015518  13.6 10439 1 AE015943 AE0105943  13.1 101439 1 AE0105977 AE0105943  13.2 12929 1 AE000577 AE0105943  13.3 316208 1 AAC0100977 AE0105943  13.3 316208 1 AAC0100977 AAC01009794  13.3 316208 1 AAC010097 AAC010097  13.3 316208 1 AAC010097 AAC010097  13.3 316208 1 AAC01009 AAC010097  13.3 316208 1 AE010455  13.0 10029 1 AE010455  13.1 10029 1 AE010455  13.1 10029 1 AE010455  13.2 124528 6 AAC01009  13.3 124528 6 AAC01009  13.4 21975 1 AE007458  13.5 122898 6 AAC01098 AAC01000  13.6 12.3 301289 1 AE0104236  13.7 10462 1 AE0104236  13.8 4802 2 AE007458  14.9 12.4 21976 6 AAC01098 AAC016236  15.1 10029 1 AE0104236  15.1 10029 1 AE0104236  15.2 12.0 4 21976 6 AAC01098 AAC016236  15.3 124521 1 AE0104236  15.4 12.4 21976 6 AAC01098 AAC016236  16.5 12.3 301289 1 AE0104000  17.6 12.2 220000 1 AE01039 AAC01638  17.6 12.2 220000 1 AE01039 AAC01638  17.6 12.2 220000 1 AE01039 AAC01639  17.7 12.2 220000 1 AE01039 AAC01039  17.7 12.2 220000 AAC01639  17.7 12.2 220000 AAC01630  17.7 12.2 220000 AAC01639  17.7 12.2 220000 AAC01630  17.7 12.2 220000 AAC01630  17.7 12.2 220000 AAC01630  17.7 12.2 220000 AAC01630  17.7 12.2 22000	13.6 13.9 347961 1 BX551657 ABC03515  13.6 13.9 13.9 147961 1 BX551657 ABC03515  13.1 101439 1 AE015943 ABC015943  13.2 10415 1 AE000977 ABC007594  13.2 10415 1 AE000977 ABC007594  13.3 31208 1 AAK417049 AK417019  13.3 31208 6 AX417049 AK417019  13.3 31208 6 AX417036 AX417019 AX417036  13.3 31208 6 AX417036 AX417019 AX417036  13.1 10738 1 AE006565 AE00666 AX61704  13.2 19841 1 AE006565 AE00666 AE00667  13.3 131650 1 AE014593 AE0114953  13.1 10738 1 AE014953 AE0110455  13.1 10738 1 AE014055 AE011045  13.1 10738 1 AE014236 AX611673  14.8 12.4 10462 BD003116 BD003116 AX6116700  13.1 10700 6 AX611678  14.8 12.3 10728 1 AX611678  15.1 10700 6 AX611668  16.1 12.2 10700 6 AX611669  17.4 12.4 12.4 10700 AX61167  18.1 12.2 12.1 1 AE017039  18.1 12.1 1 AE017039  18.1 1 AE017039  18.1 1 AE017039  18.1 1 AE017039  18.1 1 AE01		91.	٠.	34155		BX248355	Coryne
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5         83.6         13.7         30.4439         J AE0115943         AE0105943         AE0010947           6         83.6         13.5         10415         J AE0010977         AE0010947         AE0010947           7         82.4         13.5         10415         J AE0010947         AE0010394         AE0010394           8         8         8         13.3         120.0         AE010394         AE0010394         AE0010394           10         8         13.3         31200         AX410018         AX411019         AX411019           11         8         0.6         13.3         31200         AX4110018         AX4110018         AX4110018           13         31200         AX4110018         AX4110018         AX4110018         AX4110018           14         80.6         13.2         11202         AX4110018         AX4110018         AX4110018           15         80.6         13.1         10738         AX4110018         AX4110018         AX4110018           16         13.1         10728         AX4110014         AX4110018         AX4110018           17         13.1         13.1         13.1         AX6114573         AX4110018           13	13.6 13.7 301439 1 AE015943 AE015943 18.6 13.7 301439 1 AE0015943 AE0015943 18.6 10155 1 AE0015947 AE0010594 18.1 13.6 10155 1 AE001598 AE0010394 18.1 13.6 10252 1 AE001334 AE0151394 18.1 13.3 31208 6 AX413018 AX417049 18.1 13.3 349980 6 AX413018 AX417049 18.1 13.2 19841 1 SCU06166 AE006342 18.0 13.2 19841 1 SCU06166 AE006342 18.1 10029 1 AE0164953 AE006565 AE006565 18.1 10029 1 AE0164953 AE001004953 18.1 10029 1 AE0164954 AX641673 18.1 10029 1 AE0164954 AX641673 18.1 10029 1 AE0164954 AX641673 18.1 10029 1 AE016436 AE0076651 18.1 10029 1 AE016436 AE0076663 18.1 10029 1 AE016436 AE0076631 18.1 10029 1 AE0166 AE0076631 18.1 10029 1 AE01660 AE017039 AE017039 18.1 10029 1 AE01660 AE017039 AE017039 18.1 10029 1 AE01601 AE017039 AE017039 18.1 10029 1 AE01667 AE017039 AE017039 18.1 10029 1 AE017039 AE017039 AE017039 18.1 1003928 AE017039 AE017039 AE017039	13.6 13.7 301439 1 AE0015943 AE0015943 AE0019973 AE00199		83.	۳.	5431		AP003515	CLOSER
6 83 13.6 10575 1 AE000977 AE0009577 AE0009577 AE0009577 AE0009577 AE0009587 AE013394 B	83 13.6 10.75 1 AE000977 AE007598  10.4 13.5 10.415 1 AE007598 AE013394  10.8 13.3 312020 1 AE56174 AE413018  10.8 13.3 312020 1 AE56174 AE413018  10.8 13.3 349980 6 AE417036 AE413018  10.8 13.3 349980 6 AE417036 AE413018  10.8 13.1 349980 6 AE417036 AE606565  10.6 13.2 19841 1 SCU96166 SACOFFEE  10.8 13.1 10.738 1 AE006565 AE6014953  10.8 13.1 10.738 1 AE006565 AE6014953  10.8 13.1 10.738 1 AE014154 AE606156 SACOFFEE  10.8 13.1 10.738 1 AE014154 AE6014953  10.8 13.1 10.738 1 AE014154 AE6014953  10.8 13.1 10.738 1 AE014154 AE6014953  10.8 13.1 10.738 1 AE014236 AE6014154  10.9 12.1 10.8 10.8 1 AE014018  10.9 12.1 10.8 10.8 10.8 10.8 10.8 10.8 10.8 10	83 13.6 10575 1 AE000977 AE007598  10.4 13.5 10415 1 AE0013594 AE013394  10.8 13.3 312020 1 AL556174 AE013394  10.8 13.3 312020 6 AX417016  10.8 13.3 349980 6 AX417036  10.8 13.3 349980 6 AX417036  10.8 13.3 349980 6 AX417036  10.8 13.1 10738 1 AE006565  10.8 13.1 10738 1 AE014154  10.8 13.1 10738 1 AE014053  10.8 13.1 10738 1 AE014054  10.8 13.1 10738 1 AE014054  10.8 13.1 10738 1 AE014055  10.8 13.1 10738 1 AE014054  10.8 13.1 10738 1 AE014058  10.8 13.1 10738 1 AE014058  10.8 13.1 10738 1 AE014058  10.8 13.1 10738 1 AE014036  10.8 13.1 10738 1 AE017000  10.8 12.2 1278 6 AX51166  10.8 12.3 10.8 1 AE017000  10.8 12.2 10.8 1 AE017039  14.6 12.2 291804 1 AE017039  14.7 12.2 291804 1 AE017039  14.8 12.2 291804 1 AE017039  14.9 12.2 291804 1 AE017039  14.1 12.2 12.2 12.3 12.3 12.3 12.3 12.3 12		83.	<u>.</u>	30143		AE015943	CLOSUZ
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ACCESSION	AE010640 AE009951
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ORGANISM	Fusobacterium nucleatum subsp. nucleatum ATCC 25586
	Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
	Fusobacterium.
REFERENCE	1 (bases 1 to 11964)
AUTHORS	Kapatral, V., Anderson, I., Ivanova, N., Reznik, G., Los, T.,
	Lykidis, A., Bhattacharyya, A., Bartman, A., Gardner, W., Grechkin, G.,

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Kapatral, V., Anderson, I., Ivanova, N., Reznik, G., Los, T.,

Kapatral, V., Anderson, I., Ivanova, N., Reznik, G., Los, T.,

Zhu, L., Chu, L., Kogan, Y., Chaga, O., Goltsman, E., Bernal, A.,

Larsen, N., D'Souza, M., Walunas, T., Pusch, G.D., Haselkorn, R.,

Fonstein, M., Kyrpides, N. and Overbeek, R.

Direct Submission

Submitted (13-FB2-2002) Integrated Genomics, 2201 W. Campbell Park

Location/Qualifiers
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Zhu,L., Vasieva,O., Chu,L., Kogan,Y., Chaga,O., Goltsman,E., Bernal,A., Larsen,N., D'Souza,M., Walumas,T., Busch,G., Haselkorn,R., Fonstein,M., Kyrpides,N. and Overbeek,R. Genome sequence and analysis of the oral bacterium Fusobacterium
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J. Bacteriol. 184 (7), 2005-2018 (2002)

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S41553 bp DNA linear BCT 06-NOV-2003

Corynebacterium diphtheriae gravis NCTC13129, complete genome;

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Somplete genome;

Corynebacterium diphtheriae

Corynebacterium diphtheriae

Corynebacterium diphtheriae,

Corynebacterium diphtheriae

Sambacterium

Corynebacterium

SE BETATIOU, A., Dover L.G., Holden, M.T.G.,

Pallen, M., Bentley, S.D., Besta, G.S., Churcher, C., James, K.D., De

Zoysa, A., Chillingworth, T., Cronin, A., Dowd, L., Feltwell, T.,

Hamlin, N., Holroyd, S., Jagels, K., Moule, S., Quall, M.A.,

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diphtheriae NCTC13129

Mucleic Acids Res. 31 (22), 6516-6523 (2003)
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                                                                                       271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 AAGAAGGIICAACAAIIGIIGIIGIAACACAIGAIIIAAAAGIIGGAGAIGIGGCAGAGA
                                                      476 CCGGAGCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCG
                                                                                                                                                                                                                                                                                                270 CAGGAAACCTIGAIGAAGIAAAIGAAAAAATIGIIIAIAGAAAIATIAAAAACAACTICAIA
                                                                                                                                                                                                                                                                                                                                                                                                  536 ACAAAGGCGCCACCGTTGTTGTTGCTACGCACTCGCCCCTCTTCCGAGAATCAGCGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IQQLALRIPIPPIAAKREQLTAFADNTVPWSTLIGNAIGGNGKRTEFPKVTKDDIALI
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VLKDGAALDPEGLKTHCRKLLTRYKVPRTFYHFBALNKDQLGKVRRRBVQQTILIBRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        long-chain-fatty-acid--CoA ligase Fadb or Oldb or B1805 SW:LCFA ECOLI (P29212) (561 aa) fasta scores: E(): 7.8e-63, 34.69% id in 565 aa. Possible duplication of the upstream CDs: Similar to DIP0386 (568 aa) fasta scores: E(): 1.2e-164, 73.488% identity in 562 aa overlap" /codon start=1 /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVEHNPLYTAHELEGLFODHGARVAIAWDKAASTLEKLRDTTSLETIISVNMTEAMPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (3405. .4724)
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complement (4194. .4229)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Compute mental 12070386"

// Inote="FPPrintScan hit to PR00154, AMP-binding signature"
// Inote="FPPrintScan hit to PR00154, AMP-binding signature"
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/locus_tag="DIP0387"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \langle 10cus tag="DIP0388" \\ \text{note="Similar to Streptomyces coelicolor putative} \)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(5164. .6486)
/locus_tag="DIP0387"
/note="HMMPfam hit to PF00501, AMP-binding enzyme"
                                                           to Escherichia coli
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6726. .8009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain signature."
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/locus_tag="DIP0383"
/note="Low similarity to Mycobacterium tuberculosis
/note="Low similarity to Mycobacterium tuberculosis
hypothetical 19 1 kDa protein Rv0481c or MT0499 or
MTCY20G9.07c SW:Y481 MYCTU (Q11147) (174 aa) fasta scores:
Codon start=1
/trans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(2806..3171)
/locus_tag="DIP0385"
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(EMBL:Z99110) (125 aa) fasta scores: E(): 5e-11, 35:51% id
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        in 107 aa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEISDVLVSVTLLERATGAVMEVPAADLELAYRYSNLKFTGRGVVLGITLQIHTDGMS
APLRFGELARVLGHEGPHPAVQVREAVLGLRAGKGMVYNEADHDTWSAGSFFTNPIVP
ESVGDHVRSVVGDESMPCFAAGBGMVKLSAAMLIDRAGFAKGHQGPGGRVSLSTKHTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /locus tag="DIP0384"
//note="Similar to Mycobacterium tuberculosis
//note="Similar to Mycobacterium tuberculosis
UDP-N-acetylenclypytuvoylglucosamine reductase MurB or
Rv04812 or MY0500 or MYCY20G9.08 SW:WURB MYCTU (011148)
(369 aa) fasta scores: E(): 1.7e-39, 51_27% id in 353 aa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /locus tag="DIP0384"
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UDP-N-acetylenolpyruvoylglucosamine reductase, C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UDP-N-acetylenolpyruvoylglucosamine reductase MurB or
B3972 SW:MURB ECOLI (P08373) (342 aa) fasta scores: E():
3.1e-14, 31.69% id in 325 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(2809. 2820)
Jocus tag="DIP0385"
Anote="GcanRegExp hit to PS00294, Prenyl group binding lite (CAAX box)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transī_table=11
/product="Putative peptidoglycan synthesis related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALTNRGNATTDDLVALAREVRGGVMDAFGVLLEPEPVWVGVSI"
                                                                                                                                                                                                                                                                                                                                                                                                                                       product="Conserved hypothetical protein"
protein id="CAE48887.1"
db_xref="GI:38199256"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (3174, .4880)
/locus_tag="DIP0386"
complement (3174, .4880)
/locus_tag="DIP0386"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and to Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /locus_tag="DIP0384"
.676. .2809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     codon start=1
trans table=
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ALGEPROITJENIIGNSTATNONNISTEIGTIKANAVALNNOGEITLGFAKKVLKGG
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SNTPFILKGENFSTVIMPIVM"
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KRYLLINREGERKERKLIKTKELEKREPANIDVKKYMIEHRDISSINENBERGVG
KRYLLINREGERKERKLIKTREGERFRANIDVVKYMIEHRDISSINENBERGVG
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ASDVFSLFMGDEVEPRAXIQDHAKDVKHLDV"
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protein_id="CAE09175.1"
                                                                                                                                                                                                                                                                               chromosomal
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L. .1314
                                                                                                                                                                                             locus tag="WS0000"
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locus tag="WS0002"
561. .4879
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                                                                                                                                                                   gene="dnaA"
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Wolinella succinogenes
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                  AAGGTCTCAGTCATAAGTTTTTACCAGGAACAATGACAGCACTGAACTGGAGCGTCCGGTT 112
                                                                                                                                                                                                                                                                                                                                                                   TCCTTGTCGAGGATGTAGACCTTCTGAAACTCTTACGCGTAAGCAACGGTTATACAGGA 232
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     (387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          341 AAGTACTICAIGCIGITGGICTIGAGICGTICGAGGAAAAGCCAGITITIGAACICIG
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glycosyl transferase GlgA TR:Q9X9U5 (EMBL:AJ243803)
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Submitted (15-MAY-2003) Max-Plank Institut for Developmental
Biology, Spemannstr. 35, 72076 Tuebingen, GERMANY
Location/Qualifiers
                                                                                                           12;
                                                        Length 341553;
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                                                  15.1%; Score 91.8; DB 1; Length 3 49.2%; Pred. No. 1.9e-16; ive 0; Mismatches 277; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69256 cáccarcarcarcarcargadoracira 69228
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                                                                                                     Conservative
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280; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 84.6; DB 1;
Pred. No. 3.3e-14;
0; Mismatches 214;
                                                                                                                                                                                                                                                                                                                                                               /locus tag="WS0009"
complement (9802. .10917)
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db xref="GI:34482181"
                                                                                                                                                                                                                                                                                                        complement (9802. .10917)
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                                                                                               product="CYIB PROTEIN"
            locus_tag="WS0008"
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GHCFSPYLKLEGGKGVATGLGVMAVMLPLEAAIGLVVWLVVGKTLKISSLSSLIGIGA
                                                                                                           'tränslation="MRYGEMEVKNFNPEBIEWPNRNDRHYTIKITLPEFSCLCPRSG
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protein id="CAE09178.1"
db_xref="GI:34482177"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="conserved hypothetical protein"
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complement(6224. .8179)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rransI_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /locus tag="WS0007"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(9299. .9790)
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'db_xref="GI:34482176"
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897. .6220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       locus_tag="WS0005"
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                                                                                                                                                                                                                                                                                                                                                      table=11
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trans1 table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         start=1
                                                                                                                                                                                                                                                                                                                          codon_start=1
transl_table=
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194222 icaicricciccicada a concede de contrator de la contrator de con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194342 ATTACGAGCTTCTTGAGGCTTTTGGTATTGCACAAGTGGTGGAACAGAGCGTGGGCGAGC 194283
                                                                                                                                                                                                                                                                                                                                                                                                                                              194582 †CATGGGCGTGAGCGGTAGCGGAAAATCAACGCTCCTTCACACCCTCTCTACCTTA 194523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194522 Agécircifigéadérgadoritangerititridateahtecaretareaacifeceadegeeee 194463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194403
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                                                                                                                                            o'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  454
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                                                                                                                                                                                                                                                                                                         154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215 AGCAACGGITATACAGGAAAAATACGGTGGGCTATTTATTTCAAGATTATGCCTTGATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194462 AACTTTIGGAGCTTAGACGAGAAAGCTTGGCATCATCTTCCAATCTCACTATCTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              275 CCGACAGGACAGTTAAATTCAACCTTCAGCTTGCGGTGGAAAAACACAAATGGCCTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335 ITCCICAAGIACTICATGCTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTCTGGTGGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAATCCCCCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194282 TCTCTGGAGGACAACAGCAGCGCCTCTCGATCGCTAGGGTTCTCACCAAAAAACCCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 TGACTGGAGCGTCCGGGTTCAGGAAAATCGACTTTGCTCAACTGTTGGCACACTTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 AACCAAGTICCGGACAGAICCTIGICGAGGAIGTAGACCTICTGAAACTCTIACGCGTA
                                                                                                                                            Gaps
Length 347961;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="60 aa, similar to gp:AF143819 1 transposase-like orotein from Escherichia coli (402 aā); 38% identity in 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'translation="MLYTTNVIESLNSQFRKFTKTKLIFPNDVSLIKMLYLATEKVNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /trānslation="MNIIEISNLNKKYFDKVIFKDFSLSIKKGEMIAISGRSGCGKST
LIANTGLIFEKEDSGEIIDGVKNIKKINKSKLANKFLBRKISKEISPUDEFLYBENT
RLAIKHTIKNTKKIEEEIIRCLFRVGLEGCGKNYIYELSGGSGCANAIARLKFSEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="83 aa, similar to pir:T14710 probable transposase
from Yersinia pestis (402 aa); 44% identity in 50 aa
overlap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4588. .4746
/gene="PCP06"
/note="52 aa, similar to pir:T43600 probable transposase
from Yersinia pestis (105 aa); 56% identity in 50 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (5169. 5804)

complement (5169. 5804)

/gene="PCPO7"

/function="ATP-binding protein"
/note="211 aa, similar to gp:AP001508 4 ABC transporter
/note="111 aa, similar to gp:AP001508 4 ABC transporter
/note="111 aa, similar to ap.AP001508 4 ABC transporter
/note="111 aa, similar to ap.AP001508 4 ABC transporter
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                                                                       no significant homology"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            producT="probable ABC transporter"
protein id="BAB62445.1"
(db_xref="G1:15076720"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transī_table=11
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/gene="PCP07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        truncated"
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/gene="PCP04"
3773. .4024
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                                                                   'note="120 aa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1040. .4222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1040. .4222
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/gene="PCP06"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
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KIRDIIANDLALSATQVGRYERINKLIPELKAVIEGGNLTIANASEFSSLSEENQRV
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LKSENENIKKKLDSNIEERREIEGQIKIEPERKLKOMEKVILEEEKKYDKKIEDI
TKEAKENNIEKQRLKDELSKLKEKSNNEVDIKNIKNIVLULEEKKSPOKKIEDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /trānslation="MAKKFSISEGMLNGISKNTRKVEEFQAKENFKIEYINIDRIKRN
EKNFYEIVDIESLAEDIKLNGLNHNLVVRKLDNDMYELISGERRYTALSKLVNEGNKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="426 aa, similar to gpu:AF300944_3 presumptive ParB
protein from Lactococcus lactis subsplactis (242 aa); 30%
identity in 266 aa overlap
PCPO2"
                                                                                                                                                                                                                                                                    Shimizu,T., Ohtani,K., Hirakawa,H., Ohshima,K., Yamashita,A., Shiba,T., Ogasawara,N., Hattori,M., Kuhara,S. and Hayashi,H. Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-APR-2001) Tohru Shimizu, Institute of Basic Medical Sciences, University of Tukuba, Department of Microbiology; 1-1-1 Temnohdai, Tsukuba, Ibaraki 305-8575, Japan (E-mail:tshimizu@md.tsukuba.ac.jp, Tel:81-298-53-3354,
                                                                                            Clostridium perfringens str. 13
Clostridium perfringens str. 13
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="250 aa, similar to pir:140444 Spo0A activation
inhibitor soj from Bacillus subtilis (253 aa); 37%
identity in 250 aa overlap
                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99 (2), 996-1001 (2002) 21664373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'db_xref="taxon:195102"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .54310
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Location/Qualifiers
   AP003515
AP003515.1 GI:15076712
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/gene="parB"
1751, .3031
/gene="parB"
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/gene="PCP03"
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/gene="soj"
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/gene="soj"
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301439 bp DNA linear BCT 06-FEB-2003
Clostridium tetani EB8, section 8 of 10 of the complete genome.
AE015943 AE015927
AE015943.1 GI:28204047
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/protein id="%A036487.1"
/db_xref="GI:28204048"
/translation="MSRNFSVFDIVGPIMIGPSSSHTAGAARLAKLAASIAGEKIKKV
5558 ATAAGTTACTTATTTCAAAATTTTGCCTTGGTAGAAGAAAGTGTAGAGGAGAGATTTA 5499
                                                                                                                   5439
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Submitted (31-0CT-2002) Goettingen Genomics Laboratory, Institute
Submitted (31-0CT-2002) Goettingen Genomics Laboratory, Institute
Of Microbiology and Georg-August University,
Grisebachstr. 8, Goettingen 37077, Germany
Location/Qualifiers
1. 30142611
/ organism="Clostridium tetani E88"
/ forganism="Clostridium tetani E88"
/ strain="Massachusetts"
/ sub_strain="Massachusetts"
/ sub_strain="E88"
/ db_zref="taxon:212717"
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Bruggemann, H., Baumer, S., Fricke, W.F., Wiezer, A., Liesegang, H., Docker, I., Herzberg, C., Martinez-Arias, R., Merkl, R., Henne, A. and Gottschalk, G.
The genome sequence of Clostridium tetani, the causative agent of tetanus disease.
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Decker,I., Herzberg,C., Martinez-Arias,R., Merkl,R., Henne,A. and
Gottschalk,G.
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Clostridium tetani B88
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
Clostridium:
                                                                                                                   CAGCTTGCCGTGGAA------AAACACACAAATGGCCTGAAATTCCTCAA
                                                                                                                                                                                                                                                          GGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAATCCCCGAATAATTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                              523 AGAGCACTCGCCGACAAAGGCGCCACGTTGTTGTTGCTACGCACTCGCCCCTCTTCCGA
                                                                                                                                                                  343 GTACTICATGCIGITGGICTICAGICGTICGAGGAAAAGCCAGITITIGAACTCTCTGGI
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2. .778
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GNI INI SEDEKDRILLUVPEKYRNFEKILETYGYGYNSOE PCSSTTCSHKTADGKLALIVUS
GNGKI IMMKSNQKYTFGYLLDVNPEKRILETYYGYNSOE PCSSTTCSHKTADGKLALIVUS
KIRANSEBEVINGLEKYYDMSYYLIDPYNYTPEPT VSYLTESNDKLYSYTYLIGYNNSPF
KIRANSEBEVINGLEKYYDMSYYLIDPYNLYDDNASTIINIKAKWYTIIRAYULLLAV
ISIILLIQNISLIY RODNYKTIYKKKHOYRLIYRYMNYFIMVLITWTCPLAIASLITKA
INI YFTLIVVIELVYIELVYFIIRNINSLEKKNLIKKVIKGEY"
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                                                                                                    /note="720 aa, similar to gp:AP001508_3 BH0280 gene
product from Bacillus halodurans (713 aa); 23% identity in
661 aa overlap"
                                                                                                                                                                                                                                                                                     /translation="MKKKVALIILFIIITISFEGVYSVRNHTEFMKLKVLQGNLENF
EVTISIPDERNYNTAYESIIKSLDEYNGNIFFSEVDINEDNKKVINVSYFSNKKTENT
IPIVSGRFFHEKONIDSYLSTIDSEDYQQIGVINDFNGKNIHEIRTIKSKLDINTFEN
LFIVQIENGQILDKLIEDLKSESIIVQKRVMGOSSQYMTETLKIILVVCFIGLIFMIF
                                                                                                                                                                                                                                                                                                                                                                              YQVLGSYKKIGIQKLLGHSTFVMLKERLLEVLRIEVIVMLVVTVLLVFRNFKTFNSLF
WKFMLELICIYSIMIIFTIVSVIIPYIYVSKITLSNIIKNKRPVKSIIILNSIVKVIL
ASIILIFFSNALDDLSSIGKGYEKNYKVWEETKQYYILPELGFNDESIQSFSIEEMEK
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QAQSSKFYCGEQKHRATARVKVGTTLYBAKDIKDAKLTAHAQTKYYKGVTEWNSYYAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ^note="77 aa, similar to probable transposase from
fersinia pestis plasmid pMT1 (402 aa); 25% identity in 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5678 AGTACCCTTTTAAATATGATAGGCTTGATAGAAAATTTGATTCAGGAGAAAATTATT 5619
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Pred. No. 3.7e-14;
0; Mismatches 307; Indels
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product="conserved hypothetical protein"
protein_id="BAB62446.1"
db_xref="GI:15076721"
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/transl_table=11
/product="probable transposase"
/protein_id="BAB62448.1"
/db_xref="GI:15076723"
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product="hypothetical protein"
protein_id="BAB62447.1"
db_xref="G1.1507672"
                                                 complement (5804. .7966)
/gene="PCP08"
            omplement (5804. .7966)
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complement (1704. .2639)
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In breet submission

L Submitted (15-DEC-1997) The Institute for Genomic Research, 9712

Medical Center Dr. Rockville, MD 20850, USA

Nedical Center Dr. Rockville, MD 20850, USA

origin of this version has been moved by TIGR to position 2093570 of the original version and the opposite strand is shown from the original version.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Archaeoglobus fulgidus DSM 4304"
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REFERENCE
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125168 GATGGTGAAAATATAAAAATATAAATTCATCGAAATCAAATAAAAATATTAAGAGAAAA 125109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125288 TCACTAGATATACAAGATGAAGAACTCCTAGCTGTAACTGGAGCAAGTGGAAGTGGAAAA 125229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rcracharararararadgecrrrradagegrrrrgarrcregaadgerrrran 125169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125348 AITGTAAAGAIGGAGAATATAACTAAAAATITIGGAGATAAAAITATACTAAATAATTI 125289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10575 bp DNA linear BCT 17-MAR-2003
DSM 4304 section 130 of 172 of the complete
                                                                                                                                            IAKIDIKLTKKOGKYTVSDKTKUVTSKI IMMOGKTKKVNYESDKDLEKKLNSYHKVA
LDDANOI IGELKGGNLVPEDEVKGI PTSQIQETPMINLINEVQMYYTKANVSAAAFR
SNANNKQGKIKKSDASLIYKPDNTLYLLEVTGKQLKDYMSASSYYMYKPGBLTVSF
BDYRGYNYDPFSGYXYEIDISKE PGNRI INLRKMDNSLYKDTETLKLIVNNYRASSH
NLLNPNSGI PKDGSLPKLI EKDALDGTPIRDILGRYIKEVKGYITPQMNNNWLISGNN
WDSAKRKAIKAVKLIKPAGK KOPQSKDARTPNVASITEKDLENAKNKAVKPVDKKPTTK
PDSKDSKDKKVIKPADKKTVYTVKSGDCLYLIGQKYNVSYKKIAKANNIKNVNILIFVG
                                                                        PYNI VEKAGYKVGI I CMTTPNI TRWDSENLKGYRVTDPVEETKKVI SEI KDKVDVMI A
VVHNSEGEEYGNKNSSAVSLANACPELVAI VAAHEHKAVDGATYNNVLLVENKNLAQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGGATGTAGACCTTCTGAAACTCTTACGCGTAAGCAACGGTTATACAGGAAAATACG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   463 GCTGATGAACCAACCGGAGCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTG 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----AAAAACACAAATGGCCTGAAATTCCTCAA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAATCCCCGGAATAATTCTG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCGACTITGCTCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATCCTTGTC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaeoglobus fulgidus DSM 4304
Archaeoglobus fulgidus DSM 4304
Archaeoglobus rechaeocta, Archaeoglobi; Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
1 (bases 1 to 10575)
Klenk, H.P., Clayton, R.A., Tomb, J., White, O., Nelson, K.E., Ketchum, K.A., Dodson, R.J., Gwinn, M., Hickey, B.K., Peterson, J.D., Richardson, D.L., Kerlavage, A.R., Graham, D.E., Kyrpides, N.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 GTGGGCTATTTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAGTTAAATTCAACCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ATGATAGAAATCAATGACCTCAAGAAATCTTTTGGCGTTCGGATCTTATGGCAAGGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTACTTCATGCTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCCAGTTTTTGAACTCTCTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 301439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124808 AATAAACTCAACAAAAAGGAAAAACAGTAATAGTAATAATCTCA 124765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                523 AGAGCACTCGCCGACAAAGGCGCCACCGTTGTTGTTGCTACGCA 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 83.6; DB 1;
Pred. No. 6.6e-14;
0; Mismatches 284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaeoglobus fulgidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AE000977 AE000782
AE000977.1 GI:2689300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGCTTGCGGTGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                 ORLIIPAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AE000977
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCUS
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ORGANISM
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VERSION
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AUTHORS
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AE000977
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엄 ò dd ò 셤  $\delta$ g ò g ð qq ઠે 엄 ò g  $\delta$ 

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KEYWORDS

CDS

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CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
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TPLEVGFRAGFERVKKFADYYGPEFILIYEEGEEFTTPSPGSYAIVYIPEKDMKAGI
KENBELKIRVABKKERNEEILRKVLTILGDKVEEFFTTGENQVSRKLLKEDLEGFRGLAVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PER PER INVESTIGATION OF THE CONTROL OF THE CONTROL
                                                                                                            /note="similar to GB:L77117 SP:QS8206 PID:1591493 percent identity: 51.13; identified by sequence similarity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6826 CAGAGAGTIGCCAIAGCGAAGGGCTCIGGTIAAGAACCCGCCAATAATTCTCGCTGACGAG 6885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6706 AACGIGGAGATIGCAGCAGATITGGITGAGAGCCCGAGGGATGIGGATGAGGIGCTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6466 GGGATAAATCTTGAAATAGAGCGGGGAGAGTTCATGGTCGTTCTGGGCCCCTCAGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAAAATCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5586 ATTITIGAIGGIAAGGAIAICACGAATIACAAIGAAGACAGGCICACCAIGCACAGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 AATACGGTGGGCTATTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAGTTAAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTGTCGAGGATGTAGACCTTCTGAAACTCTACGCGTAAGCAACGGTTATACAGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="hypothetical protein; identified by GeneMark;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cch 13.6%; Score 83; DB 1; Length 105 al Similarity 49.1%; Pred. No. 4.3e-14; 249; Conservative 0; Mismatches 255; Indels
                                                                                                                                                                                                                                                                                                                         table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7031. .9406
/gene="AF1820"
7031. .9406
/gene="AF1820"
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/codon_start=1
/transl_table=1:
                                                           gene="AF1819"
                                                                                                                                                                                                                                                             /codon_start=1/transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S:
Matches 249
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EDRLKNCSFKI VGTVTSPLYI SAQRQI SSVGNGNVKGFVYIMPEAFKNDVYTSI YVKI
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Childress, D., Zeng, Q. and Smith, D.R.
Direct Sibmission
Submitted (24-UUL-2001) GTC Sequencing Center Production,
Finishing, and Bioinformatics teams, Genome Therapeutics (crp., 100
Beaver Street, Waltham, MA 02453-8443, USA
Location/Qualifiers
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DDIAIILREKKNKTQVRKLIVNLIDIFYGNIIDKLDIQEI"
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472 CCAACCGGAGCTCTAGATTTAACAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTC 531
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Nolling, J., Breton, G., Omelchenko, M.V., Markarova, K.S., Zeng, D., Sibson, R., Lee, H.M., Dubois, J., Qiu, D., Hitti, J., Wolf, Y.I., Tatuson, R.L., Sabathe, P., Doucette-Stamm, L., Soucaille, P., Daly, M.J., Bennett, G.N., Koonin, E.V. and Smith, D.R. Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum
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Clostridium acetobutylicum
Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
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VIKFKVTYLKGNTIHLTNISSLSSYSYVRLDN"
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Deppenmeier, U., Obhan, A., Hartsch, T., Merkl, R., Schmitz, R.A.,
Martinez-Arias, R., Henne, A., Wiecer, A., Baeumer, S., Jacobi, C.,
Brueggemann, H., Lienard, T., Christmann, A., Boemecke, M., Steckel, S.,
Bhattacharyya, A., Lykidis, A., Overbeek, R., Klenk, H.-P.,
Gunsalus, R.P., Fritz, H.-J. and Gottschalk, G.
The genome of Methanosarcina mazei: evidence for lateral gene
transfer between bacteria and archaea
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COMPLEMENT (4905. .5342)
Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
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/strain="Goel"
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Location/Qualifiers
1. .12929
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Best Local
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Ashdaksqrilempeeelfrvsevnieppekaliyptvicskcgegfmeplgrvknge
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                                                                                                                                                                                                              /product="tungsten formylmethanofuran dehydrogenase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="ABC transporter, ATP-binding protein"
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                                                                                   complement (5335. .5853)
                                                                                                                           complement (5335, .5853)
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10268 CATAGGCACACTTGAAAAGCCACTGACGGAAAAATACTTGTTGACGGGACAGACCTTAC 10209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .0148 GCACTACAACCTGATTCCTACACTTTCAGCCCTTGAAAACGTTGAACTTGCCATGCGCTT 10089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypochetical binding protein of ABC transporter"
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KQILGVPPEKSSVALNPVQLKAGRFLDPGDSYSVVVGNNIKREVNLEIGSKFEIHDKY
FTVVGILDYTGSIFDNAVIIPLETAQDLYSVGNSVSYIFAVPDDRVDAEMLSKRIELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKGTSTLSPGBLEVOAROSFNIFSVTIISSGLLAAIIGGLCVNNTMLMSVABETREFG
ILKAIGAETKDILLLTLGEASLMGLLGGILGIIVGIGAVQINNAWLATTRIVLFLITP
RLLIIAMLFALLIGALSGLYPAYRASKMSPMBALKHA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEBENENRIIIGFFSDHDLSDATVRFEBPHENVSLVFTLSSGKETLKSETFHLVVSVKK
DOBIGSKYPFWELEBPGKONDSYTAGLEVKGEODILBTWKFSPSRNBHLSNLKVVDF
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KKD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9908 TGAGGTCGATAGCAAAACAAGGGACTCCGTTGTGCAGATTTTTAAGGAATTGAGCCAGAA 9849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360 TCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACAAC 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 AGATTATGCCTTGATTCCCGACAGGACAGTTAAATTCCAACCTTCAGCTTGCGGTGG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10028 GCTGGAAGACCGGCTCAATCATAAACCTACGGAGCTCTCAGGTGGAGACAGAAAGGGT
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Pred. No. 9.3e-14;
0, Mismatches 235; Indels 1
                                                                               complement (10455. .11570)
                                                                                                                                                               complement (10455. .11570)
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                                            AKECSRVLRITDGMIKDH"
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complement (6307. 7917)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QWAMQANPPNDAMFRRAKNMERALERMEKVKRPVLTGKQMQLQPDEASRSGQDVVWE
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CDS
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L. Science 294 (5543), 849-852 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALS96174. 96208 bp DNA linear BCT 06-JUN-2002 Listeria innocua Clip11262 complete genome, segment 12/12. ALS96174 ALS96174 ALS92022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glaser, P., Frangell, and Rusniok, C.
Direct Submission
Submitted (09-7011-2001) Glaser P., Institut Pasteur, Genomique des
Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris
Cedex 15, FRANCE
E-mail: pglaseregesteur.fr
E-mail: 991aseregesteur.fr
Phone: +33 (0)1 45 68 89 96, Fax: +33 (0)1 45 68 87 86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Listeria innocua
Bacteria, Firmicutes, Bacillales, Listeriaceae, Listeria.
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TITLE
JOURNAL
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VERSION
KEYWORDS
SOURCE
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                                                        19689 Acaacecrecraalgererriarcecacecracarecaaagaracreccaagrarrarr
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                                                                                                                                                                                                                                                                                                                                                               361 CTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACGAACT
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Listeria inocus, genome and applications
Patent: WO 0228891-A 4040 11-APR-2002;
INSTITUT PASTEUR (FR); CENTRE NATIONAL DE SCIENTIFIQUE (CNRS) (FR)
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Llarity 47.2%; Pred. No. 5e-13;
Conservative 0; Mismatches 312;
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Best Local Simi
Matches 284;
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APELLPGDTELLKKGKPDFMGVNYYRSMTHAFNGKDGVGSGKMNTTGEKGTSEETGVP
GLYKRYNNYPYLEKTRMDWDIDPTGLR IGLRR LITNRYKLPIMITENGLGEYDSLTEDHK
IHDBYR IBYI RAHALA IQBA I TDGYBMLGYCTWSFTDLLSWLNGYQKRYGFVYVDRDE
NDEKELKRYKKDSFYWYKKTI EANGANLVEEQGK"
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NTALFFRODDLLCGLTSIGAFPIVYPTYTVDNASYMTIFFLGAQGEPVALIVALIT
GEVFSELARSPRLAMINGAPOVPPAVARSFKVLIPVIITLILESVINYLITLIABGIANIT
DLVYTVIQAPLKDMGTNVFSVIITGLVSNLLWVLGIHGPNTVAAIRDTIFTEPNLDNL
SYVORIGARMGAPYPAVMAGLINDGFAXTGGSGAMTLGLIAIFTTARRADXRDIAKLSL
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PGARREKYTLNETTYMLVLRRQYAQLTGRPLKEITGEBIFANYDAHDPISERLINEF
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jucose kinase"
codon start=1
'transi_table=11
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codon start=1
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protein_id="CAC98130.1"
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Pred. No. 3.7e-13;
0; Mismatches 312; Indels 6;
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db_xref="G1:16415448"
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/gene="lin2906"
/oc58. .1025
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/gene="lin2906"
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/gene="lin2905"
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/gene="lin2907"
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12497. .12503
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/gene="lin2908"
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/db_rref="taxon:1642"
/note="seq 9 splitted in 3 part.~seq 9: 1 to 349980-seq
4027: 300001 to 649980~seq 4028: 600001 to 684707"
                                                                                                                                                          346065 TCTCTTTCTATTGGAGCTGGCGAATTTATTGCAGTCGTCGGCGAGAGTGGTAGTGGGAAG
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                                         1 ATCATAGAAATCAATGACCTCAAGAAATCTTTTGGCGTTCGGATCTTATGGCAAGGTCTC
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Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria
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Patent: WO 0228891-A 4027 11-APR-2002;
INSTITUT PASTEUR (FR); CENTRE NATIONAL DE
SCIENTIFIQUE (CMRS) (FR)
Location/Qualifiers
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Sequence 4027 from Patent WO0228891.
AX417036 GI:21449646
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/db_xref="teaxon:1642"
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seq 9 from 1 to 349980-seq 4027 = old seq 9 from 300000 to
649980-seq 4028 = old seq 9 from 600000 to 684707"
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Listeria innocua
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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Listeria inocua, genome and applications
Patenr: WO 0228891-A 9 11-APR-2002;
INSTITUT PASTEUR (FR.), CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE (CNRS) (FR.)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 349980;
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Pred. No. 5.1e-13;
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Sequence 9 from Patent WO0228891.
AX413018
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Best Local Similarity
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AX413018
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TITLE
JOURNAL
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LLEFGTRRAQEMDAAIWGTRAAIIGGADATSNVRAKIFGLKASGTHAHALVQSYGND
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TWLSHLFGASVGREGVAVQIGGVIGHAIGKKLSAKEAKKILLITGMAAGFAGLFQTPI
AATFFAIEIIMLGKIEYRALIPALVGSYVASWTSSSLGLEKFSFAINTNIHIDPLVLL
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GLGTNLISLSFNGGHINGYDWILKLIFTVLSISAGFQGGEVTPLFAIGSTLGAALAML
FGLPVEFVAAAGYVSIFSAATNSYFGPIFIAAEVFGFGSVQYILPIMTIAYVLNGNSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="EVIDENCE BY HOMOLOGY BIO15.01 HYPOTHETICAL.General"
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                                                                                       organism="Lactococcus lactis subsp. lactis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conserved. probably nicotinic acid
phosphoribosyltransferase, evidenced by
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transI_table=11
product="HYPOTHETICAL PROTEIN"
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transI_table=11
product="HYPOTHETICAL_PROTEIN"
Jouy en Josas 78352, France
Location/Qualifiers
1. .11551
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complement(1773, .2360)
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/gene="ylaE"
                                                                                                                /mol_type="genomic DNA'
/strain="IL1403"
                                                                                                                                                                           /sub_species="lactis"
/db_xref="taxon:1360"
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/note="EVIDENCE
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/transl +=-
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|gene="ylaF"
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Bolotin,A., Wincker,P., Mauger,S., Jaillon,O., Malarme,K.,
Weissenbach,J., Ehrlich,S.D. and Sorokin,A.
Direct Submission
Submitted (09-JAN-2001) INRA, Genetique Microbienne, Domaine de
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                                           6; Gaps
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1 (bases 1 to 11551)

Bolotin,A., Wincker,P., Mauger,S., Jaillon,O., Malarme,K., Weissenbach,J., Ehrlich,S.D. and Sorokin,A.

The complete genome sequence of the lactic acid bacterium
Lactococcus lactis ssp. lactis IL1403

Genome Res. 11 (5), 731-753 (2001)
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                                           Indels
               Pred. No. 5.1e-13;
0; Mismatches 312;
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Lactococcus lactis subsp. lactis
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AE006342 AE005176
AE006342.1 GI:12724053
            47.28;
               al Similarity 47.2
284; Conservative
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REFERENCE
AUTHORS
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /noce="EVIDENCE BY HOWOLOGY BIO02.09 Riboflavin and cobalamin. 43% identical to cobyric acid synthase CobQ Heliobacillus mobilis, cobalamin biosynthesis pathway"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="ylbD"
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Best Local S
Matches 246
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KADDLKKVRAKVSDYLNQQMQSD YNFGVLNLOGEPERQLDINUQSNFVLLAGIASI SL
LVGGIGVMIMILVSTPERFRI GIKKALGARRKI LAGGRRLPSVSNFSSLGNFSFTSR
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STNQFNAFIGIDLRHYESRNFLAKEHITKRGNPYARKILFKCIHNIASASHTNPCHIA
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SVSQSVEDQAASQSVSVSQSASASQSASVSQSASASQSASAPTSVSAAARASASVSS
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complement(6301. .16446)
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contains cell wall anchor motif for gram-positive cocci
cell surface protein; contains two amino acid repeat
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/db_xref="G1:2822199"
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/codon_start=1
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/note="ORF8"
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gene="tptD"
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/gene="tptD'
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                                                                           BCT 03-APR-2000
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OTAGTİTSMNEDLPTQSKAKKEBETFIEIMDKSKTLİKGSVSEFDREKLSVGQRVDVV
           Streptococcus crista ATP-binding cassette lipoprotein (tptA), ATP-binding cassette lipoprotein (tptA), ATP-binding cassette transporter-like protein (tptB), ATP-binding cassette protein (tptC) and ATP-binding cassette transporter-like protein (tptB) genes, complete cds and unknown genes.
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4 (bases 1 to 1984)
4 (bases 1 to 1984)
5 (bases 1 to 1984)
6 (bases 1 to 1984)
7 (bases 2 to 1984)
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7 (bases 2 to 1984)
8 (bases 3 to 1984)
8 (bases 4 to 1984)
8 (bases 2000) Microbiology, University of Pennsylvania, PA 10 Locust, Philadelphia, PA 19104-6002, USA
8 (bases by submitter on before Mar 31, 2000 this sequence version replaced gi:6984159, gi:282196.
8 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 2000) 1 (bases 200
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protein id="AAB97960.1"
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Correia,F.E., Lamont,R., Bayer,M., Rosan,B. and DiRienzo,J.M.
Cloning and Sequencing of a Mutated Locus that Affects Fimbrial
Tuft Organization and Corncob Formation in Streptococcus crista
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2 (bases 4397 to 19941)
2 Octreia, F.P., Allen, T.W. and DiRienzo, J.M.
High molecular weight serine-rich protein gene (srpA) from Streptococcus crista
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/codon start=1
/transl_table=11
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/note="B15 locus"
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Correia, F.F. and DiRienzo, J.M.
Direct Submission
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899. .2164
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2 (bases 1 to 10738)

RS Ferretti, 7.J., McShan, W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux(C., Sezate,S.S., Surorcv,A.N., Kenton,S., Lai,H., Lin,S., Qian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J., Yuan,X., Olifton,S.W., Roe,B.A. and McLaughlin,R.E.

1 van,X., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J., Yuan,X., Olifton,S.W., Roe,B.A. and McLaughlin,R.E.

1 van,X., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J., Vin,A.D., Yuan,X., Olifton,S.W., Roe,B.A. and McLaughlin,R.E.

2 birect Submission

3 Location/Qualifiers

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ABCOGESS ABCOGAS2 ABCOGSS ABCOGSS I GI:13622379
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1 (bases 1 to 10738)
Ferretti,J.J., McShan,W.M., Adjic,D., Savic,D., Savic,G., Lyon,K., Primeaux,C., Sezate,S.S., Surorov,A.N., Kenton,S., Lai,H., Lin,S., Oian,Y., Jia,H.G., Najar,F.Z., Ren,Q., Zhu,H., Song,L., White,J., Yuan,X., Clifton,S.W., Roe,B.A. and McLaughlin,R.E. Complete genome sequence of an M1 strain of Streptococcus pyogenes Droc. Natl. Acad. Sci. U.S.A. 98 (8), 4658-4663 (2001)
                                                             2491
                                                                                                                                                                                                                                                                                                                                                                                       2612 TGCTCTGGTGACCAATCCCAGCTTTATTCTGGAAGAACGAGCCAACTGGAGCGCTGGATAC 2671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2672 ciagaicciditiciagaicaligaigatathaacaathaacaaacaaadha ar 2731
                                                                                                                                             431
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                                                                                                                                                                                                                                       372 cgaggaaaagccagririrgaacrcrcrqqrqqcgaacaacaacqaacqaacrq
                                                                                                                                                                                                                                                                        492 AACAAACAGTGAGGTAGTCATAGAAGCATTGAGAGCACTGGGCGACAAAGGCGGCCAGCGT
GATTCCCGACAGACAGTTAAATTCAACCTTCAGCTTGCGGTGGAAAAACACAAATGGCC
                                                                                                                           recreasgracineargergracingagregit
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Streptococcus pyogenes M1 GAS
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             552 IGITGITGCTACGCACTCGCC 572
                                                                                                                                 330 TGAAAT----
                  270
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VERSION
KEYWORDS
SOURCE
ORGANISM
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AE006565/c
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DEFINITION
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Page 22

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transT_table=11
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ATP-binding protein - Thermotoga maritima (strain MSB8)
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transporter, ATP-binding protein [Thermotoga maritima]"
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/note="The N-terminal amino acid sequence of this ORF has note="The N-terminal from a spot isolated by 2-D gel ben determined from a spot isolated by 2-D gel bent crophoresis from another strain of S. pyogenes. Hogan, D. A., Whitton, M. M., Rogers, J. and R. A. VanBogelen. 2000. Two-dimensional gel electrophoresis map of Streptrococcus pyogenes proteins. Unpublished data.; Best Blastp hit = emb|CAAO3877.1| (AJ000042) gls24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MMEKTQIKSTLTYDDKVIEKIVGHALENVGGLLAVTGGFFSNIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NNLVNSESVTDGVSVEVGSKEVAVDLAIIVBYGKDIPAIAESIKAIVSQNVDSMTHLK
VVEVNVVVDIRTKEEHEAASVTVQDRVTSAASSTSGFVSEQTEKLKDTISDTVNSDE
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(Bacillus halodurans) >gi|10172996|dbj|BAB04102.1|
(AP001508) transcriptional regulator (GntR family)
[Bacillus halodurans]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'trans] table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /producT="conserved hypothetical protein"
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                                                                                complement (5832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="SPy1258"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5651. .7193
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                                                                                CDS
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gene

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Best Local Similarity 49.0%; Pred. No. 3.7e-13;
Matches 243; Conservative 0; Mismatches 250; Indels
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July 30, 2004, 06:49:19; Search time 450 Seconds (without alignments) 5749.228 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on:

US-09-868-338-7\_COPY\_1117\_1725 609 1 atgatagaaatcaatgacct.......cggataccattatcaaacta 609 Title: Perfect score: Sequence:

3373863 seqs, 2124099041 residues IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table: Searched:

Total number of hits satisfying chosen parameters:

6747726

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

N\_Geneseq\_29Jan04:\*

1: geneseqn1980s:\*

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9: geneseqn2003s:\*

10: geneseqn2003s:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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Description	Aaa65395 Brevibact	Continuation (4 of	Continuation (30 o	Continuation (12 o	Aav65222 DNA encod	Abn66720 Streptoco	Continuation (29 o	Aas55747 Streptoco	Abn67102 Streptoco	Continuation (10 o	Abx07412 S. pneumo	Aav52169 Streptoco	Continuation (15 o	Abq71073 Listeria	Aca39374 Prokaryot	Acc69145 M. genita	Continuation (6 of	Aat58840 Mycoplasm	Continuation (13 o	Aca46798 Prokaryot	Continuation (7 of	Abg71007 Listeria	Aca42947 Prokaryot
ΠD	AAA65395	ABQ67196 3	ABQ69245_29	ABA90521_11	AAV65222	ABN66720	ABA03041_28	AAS55747	ABN67102	ABN71527_09	ABX07412	AAV52169	ABS56454 14	ABQ71073	ACA39374	ACC69145	AAT58840 5	AAT58840_0	ABA03041_12	ACA46798	ABA90521 06	ABQ71007	ACA42947
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Score	609	80.8	80.8	80.6	80.4	80	79.2	77.4	75.6	75.6	75.4	75.4	75.4	75	74.6	74.6	74.6	74.6	74.6	74.4	74.4	73.6	73.2
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## ALIGNMENTS

Brevibacterium lactofermentum gltBD gene DNA sequence SEQ ID NO:7. Brevibacterium lactofermentum; ABC transporter; breeding; ATPase; corynebacterium; gltBD; L-glutamic acid; ds. AAA65395 standard; DNA; 2370 BP. (first entry) (revised) 15-SEP-2003 09-NOV-2000 AAA65395; RESULT 1 

Corynebacterium glutamicum, Key CDS

Location/Qualifiers
1. .1104
/\*tag= a /\*tag= a /\*tag= b /\*tag= b /\*product= "ORF2"
1117. .1728
/\*tag= c /\*tag= c /\*tag= c /\*tag= c /\*tag= c /\*tag= c /\*product= "ORF3" 99WO-JP007079. WO200037647-A1 16-DEC-1999; 29-JUN-2000. CDS

Kanno S, Kimura E, Matsui K, Nakamatsu T;

98JP-00360621.

18-DEC-1998;

(AJIN ) AJINOMOTO CO INC.

WPI; 2000-452189/39. P-PSDB; AAB12591, AAB12592, AAB12593.

ABC transporter constituent of Brevibacterium lactofermentum, its encoded gene and variants, applicable in breeding Corynebacteria particularly for production of L-glutamic acid.

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of ABO69245 from base 2900001 (Listeria innocua DNA sequence #684)
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           Length 110000;
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           Score 80.8; DB 6;
Pred. No. 8.3e-15;
0; Mismatches 312;
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                          The present invention describes a protein (I) which can be used to construct an ATP binding cassette (ARC) transporter. ABC transporter DNAs can be used in breeding Corynebacteria particularly for production of L-glutamic acid. The present sequence encodes three ORPs (open reading frames) from the Brevibacterium lactofermentum gltBD gene, which is used in the exemplification of the present invention. (Updated on 15-SEP-2003 to standardise OS field)
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Pred. No. 2.2e-191;
0; Mismatches 0; Indels 0
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P Sequence split into 7
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P ABQ67196 1
P ABQ67196 2
P ABQ67196 4
P ABQ67196 4
P ABQ67196 4
P ABQ67196 6
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ABQ67196 3
Continuation (
WP Sequence sp
WP ABQ6719
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Marsossilos   Second   Secon	SULT 5 V65223/C AAV65222 standard, DNA; 1010 BP. AAV65222; 24-DEC-1998 (first entry) DNA encoding a S. pneumoniae transpor Streptococcus pneumoniae protein; recvirulence; antibody; infection; detection; detect
ABG69245-1 ABG69245-2	Cy 601 AT 602  Db 34215 AT 34214  RESULT 4  ABA90521 11  Continuation (12 of 24) of ABA90521 from base 1100001 (Genomic sequence of Lactococcus l Continuation (12 of 24) of ABA90521 from base 1100001 (Genomic sequence of Lactococcus l WP Sequence split into 24 fragments Locus ABA90521 Accession Aba90521  WP ABA90521 01  WP ABA90521 01 100001 210000  WP ABA90521 03 300001 310000  WP ABA90521 04 400001 510000

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587 CGACTGGAGCCTTGGATTATCAGACGGGCAAGCAGGTTTTGAAA 544
                                                                                     BP.
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24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                                                                                                                                               29-OCT-2001; 2001WO-GB004789.
                                                                                     DNA; 711
                                                                                                                                             01-JUL-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 49.0
Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                             Streptococcus pyogenes.
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                                                                                      ABN66720 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; ABP26089.
                                                                                                                                                                                                                                                                                        WO200234771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Telford J,
Tettelin H;
                                                                                                                 ABN66720;
                                                           RESULT 6
                                                                          ABN66720
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                                                                                                                                                                                                                                                                                                                                                          This DNA sequence encodes a Streptococcus pneumoniae transport protein. The invention provides DNA sequences (AAV65201 to AAV65304) from the Streptococcus pneumoniae genome and corresponding protein sequences (AAAW80605 to AAAW80728). A recombinant host contraining a vector comprising any of the above nucleic acids can be used for the recombinant expression of the protein sequences. The invention also provides a DNA chip having arrayed on it at least 15 base pair fragment of any one or more of these DNA sequences. The DNA chip can be used methods for evaluating gene but sepression in S. pneumoniae and for identifying virulence genes in S. pneumoniae and for identifying virulence genes in S. pneumoniae and to the above proteins or peptide fragments can be used to treat S. pneumoniae infection. The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115 GGAAAATCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACCTICAGCTIGGGGIGGAAAAACACAAAIGGCCTGAAATIC--CTCAAGIACTICAIG 352
                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae nucleic acid sequences - used in DNA chips for evaluating gene expression, and identification of virulence genes.
                                                                                                                                                                                       SR;
Skatrud PL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       947 decaaercaacaerrerraacerrerresessaresaraceargareaarsaresaare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 CTTGTCGAGGATGTAGACCTTCTGAAACTCTCTACGCGTAAGCAACGGTTATACAGGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           353 CTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 80.4; DB 2; Length 1010;
Pred. No. 9.9e-16;
0; Mismatches 231; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1010 BP; 285 A; 247 C; 207 G; 271 T; 0 U; 0 Other;
                                                                                                                                                                                   Dehoff BS, Hoskins JA, Jaskunas
Peery RB, Rockey PK, Rosteck PR,
J, Treadway PJ, Young Bellido ML;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide fragments can be used to treat'S. pneumoniae infer
antibodies can also be used to detect S. pneumoniae cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        473 CAACCGGAGCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAA 516
                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 63; 333pp; English.
                                                                                                    97WO-US022578,
                                                                                                                              96US-0036281P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 49.8%;
Matches 231; Conservative
                                                                                                                                                                                                                   Solenberg PJ,
                   Streptococcus pneumoniae
                                                                                                                                                                                      Burgett SG,
Norris FH,
                                                                                                                                                         (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                              WPI; 1998-348529/30.
                                                                                                                                                                                                                                                             P-PSDB; AAW80648
                                                                                                                               13-DEC-1996;
                                                                                                    09-DEC-1997;
                                            WO9826072-A1
                                                                                                                                                                                      Baltz RH,
Mills BJ,
Smith MC,
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 54813 sequences (S1), given in the specification. The proteins have antibacterial and antihilammatory activity. (I), nucleic acids encoding (I), ABM66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a Streptococcus ample (I) is used to detectmine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used to a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chemical and distinguishing/identifying
                                                                                                 Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antinflammatory; infection; vaccine; meningitis; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Streptococcus protein for the treatment or prevention of infection disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
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Streptococcus polynucleotide SEQ ID NO 1353
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OY 1 ATGATAGAAATGAACTCAAGAAATCTTTTGGGTTCGGATCTTATGGCAAGGTCTC 60	OY 61 AGTCATAAGTTTTTACCAGGAACAATGACAGCACTGACTG	QY 121 TGGACTTTGCTCAACTGTCTTGGCACACTTGACAAGCCAAGTTCCGGACAGATCCTTGTC 180  Db 58083 ACCACGCTGCTAAATGTTATCGGACACATCAAAAGATAGTGGGGCAAGTTATTATT 58024	OY 181 GAGGATGTAGACCTTCTGAAACTCTCTAGGGGTAAGCAAGGTTATACAGGAAAAATAGG 240  Db 58023 AACGAGATGGAATATCAGACGAAAAAAGGGTTATGACTCTAAAAAAAAAA	QY 241 GTGGGCTATTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAGTTAAATTCAACCTT 300  Db 57969 TTAGGTTTATATTTCCAAAATTATCTATTGATGGAAAATGAAACAGTGTTAGAAAACTTA 57910	Qy 301 CAGCTTGCGGTGGAAAACACAAATGGCCTGAAATTCCTCAAGTACTTCATGCTGTTGGT 360 Db 57909 TCCATTACAGGTGGGGAAAATGCCAAGCTGATGATGATGATGATGAAGAAGTAGAAGAAGTAGAAATG 57850	OY 361 CTTGAGTCGTTCGAGGAAAAGCCAGTTTTGAACTCTCTGGTGGCGAACAACAACAACT 420	OY 421 GGGTTGGCCGGGTACTGCTCAAAATCCCCGAATAATTCTGGCTGATGAACCGAACCGGA 480	OY 481 GCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCGACAAA 540	Db 57669 GGTAAGACTATCGTTTACGCATGACCCAGAAATATCTGCAAAAGCAGATCGAATC 57610 Qy 601 AT 602	Db 57609 AT 57608	SULT 8 S55747	<b>\$ \$</b>	XX DT 13-FEB-2002 (first entry) XX	DE Streptococcus pneumoniae DNA for cellular proliferation protein #318. XX	KW Antisense, ds, prokaryotic cellular proliferation gene, antibiotic, KW antibacterial, drug design.	AA OS Streptococcus pneumoniae. vy	EN WO200170955-A2. XX	PD 27-SEP-2001. XX	21-MAR-2001;	21-MAR-2000; 23-MAY-2000;	PR 25-OCT-2000; 2000US-024172FP. PR 27-NOV-2000; 2000US-0253625P. PR 27-NOV-2000; 2000US-0253625P. PR 12-PGC-2000; 2000US-0253731P. PR 16-FFR-2001; 2000US-0253931P.	1
Qy 126 TTTGCTCAACTGTCGAGACAAACCAAGTTCGGGACAGATCCTTGTCGAGGA 185	OY 186 TGTAGACCTTCTGAAACTCTCTACGCGTAAGCACGCTTATACAGGAAAATACGGTGGG 245  Db 216 CAAAGACATTGCTCATTACACGTCTAAGCCTTAACTCAGTATCGTCGGAATGCTTGG 275	QY 246 CTATITATITCAAGAITATGCCTIGATICCCGACAGGACAG	OY 306 TGCGGTGGAAAACACAAATGCCTGAAATTCCTCAAGTACTTCATGCTGTTGGTCT 362.  Db 336 AGCAGTTGAAATTGTAGCGTTAAAATCCTGTGACCATTTAAAGGAAGTAGGACT 395	Qy 363 TGAGTCGTTCGAGGAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACGAACG	Qy 423 GTTGGCCCGGGTACTGCTCAAAAATCCCCGAATAATTCTGGCTGATGAACCAACC	OY 483 TCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCGACAAAGG 542	0y 543 CGCCACCGTTGTTGTT 558	VUT 7 03041_28/c trinuation (29 of 30) of ABA03041 Sequence split into 30 fragments	<b>o</b>	ABA03041_03 300001 ABA03041_04 400001 ABA03041_05 500001	ABACSO41 05 600001 ABACSO41 07 700001 ABACSO41 08 600001	ABA03041_09 900001 ABA03041_10 1000001 ABA03041_11 1100001	ABA03041 12 1200001 ABA03041 13 1300001 ABA03041 14 1400001	ABA03041_15 1500001 ABA03041_15 1500001	ABA03041_17 1700001 ABA03041_18 1800001	ABA03041_19 1900001 ABA03041_20 2000001 ABA03041_21 2100001	ABA03041_22 2200001 ABA03041_23 2300001	ABA03041 24 2400001 ABA03041 25 2500001	ABA03041 26 2600001 ABA03041 27 2700001	ABA03041_28 2800001 ABA03041_29 2900001	Query Match 13.0%; Score 79.2; DB 6; Length 110000; Best Local Similarity 47.0%; Pred. No. 2.8e-14; Matches 283; Conservative 0; Mismatches 313; Indels 6; Gaps 1;	

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WPI; 2001-611495/70
           P-PSDB; AAU37888
    Haselbeck R,
Yamamoto RT,
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ABN67102 standard; DNA; 750 BP.
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ABN67102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Eschericial coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins and to obtain antibodies capable of binding to the express these proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The used to screen compounds in rational drug discovery programmes. The busic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent call not form part of the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           442 cagcicaercicarricacicacicaciana de anticorana de cagcicarda de composica de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicación de composicaci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322 AArgiggAaciggcrrcrgAAArrgaacAgArgccrigAarrcrgAcAgacrrgAcA
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                                                                                                                        Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
                                                                                                                                                                                                                                                                                                                                                         polynucleotides for the identification and development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 12.7%; Score 77.4; DB 4; Length 711; Best Local Similarity 50.8%; Pred. No. 8.2e-15; Matches 236; Conservative 0; Mismatches 226; Indels 3
                                                                                                                    Ohlsen KL, Zyskind JW, Wall D, Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                   antibiotics, comprise sequences of antisense nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 711 BP; 187 A; 132 C; 190 G; 202 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 27; SEQ ID NO 9384; 511pp; English
                                             (ELIT-) ELITRA PHARM INC
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The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GBS (Streptococcus gagalactiae) or group A streptococcus/GBS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABM66044-ABM7126 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be mingitis. Nucleic scidenceding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromosomy and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 rogogadadacidericiecradatarirringeractringdadadecedacaarigedea 192
                                                                    Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; gene; antiinflammatory; infection; vaccine; meningitis; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 caagacerceartriraagrigaacaaggegaarricarrecrarrargegagagricregr
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48.3%; Pred. No. 3.3e-14;
tive 0; Mismatches 259; Indels 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grandi G,
Streptococcus polynucleotide SEQ ID NO 2117.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; Page 3364; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-OCT-2001; 2001WO-GB004789
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Best Local Similarity 48.3
Matches 259; Conservative
                                                                                                                                                                                                                                          Streptococcus agalactiae.
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P-PSDB; ABP26471.
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Tettelin H;
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172 ATCCTTGTCGAGGATGTAGACCTTCTGAAACTCTTACGCGTAAGCAACGGTTATACAGG 231

RESULT 9

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51908 TIGAAAAATCTTGGTTTTCGTCTTTCAGACTTCAACCTTTTGGATACTCTCTGTAAGA 51967
                                                                        51968 GATAATATCTATCTTCCTTTAGTTCTTGATCGTAAACGTTACAAAGAAATGGATCATCGT 52027
                                                                                                                                                                                          52148 ATTTTATTAGCAGATGAACCAACAGCAGCGTTAGATTACCGTAATTCAGAAGACTTGCTG 52207
                                                                                                    334 ATTCCTCAAGTACTTCATGCTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAA 393
                                                                                                                                                                                                                      454 ATAATICIGGCIGAIGAACCAACCGGAGCICIAGAITITAACAAACAGIGAGCIAGICAIA 513
                                             -----AAAAACACAAATGGCCTGAA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS56454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid cited above or fragments between nucleotides 8-100 of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media cear infection.
                                                                                                                                                                                                                                                                                                           52208 AATTTATTTGAAACTATTAACTTGGATGGACAAACTATTTTGATGGTAACCCATTC 52263
                                                                                                                               52028 Tigrcagaariarcircicarcigagaarigargacirarragarahagagacrificgag
                                                                                                                                                              CTCTCTGGTGGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAATCCCCGA
                                                                                                                                                                                                                                                                               514 GAAGCATTGAGAGCACTCGCCGACAAAGGCGCCACCGTTGTTGTTGCTACGCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene, ds; bacterial meningitis; pneumonia; sepsis; otitis media;
ear infection; antiinflammatory; antibacterial; immunostimulant;

    S. pneumoniae type 4 strain coding region #1700.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               auditory; respiratory; gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pneumoniae; type 4 strain.
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                                              Trcaacctrcagcrracagrag-
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                                                                                                                                                                                                                                                                                                                                                                                    ABX07412 standard; DNA; 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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(GENO-) INST GENOMIC RES
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11-FEB-2003
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GIGATTITAAAIGGGGAAGATATTACGAAAATITAAGAGGAAAATTAGCGAGITTTCGT 252
                                              291
                                                                          312
                                                                                                                                   GATAATATCTATCTTCCTTTAGTTCTTGATCGTAAACGTTACAAAGAAATGGATCATCGT 372
                                                                                                                                                               ATTCCTCAAGTACTTCATGCTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAA 393
                                                                                                                                                                                          TIGICAGAATTATCTICTCATCTGAGAATTGATGACTTATTAGATAAGAGACCTTTCGAG 432
                                                                                                                                                                                                                                                   ATTTTATTAGCAGATGAACCAACAGCAGCGTTAGATTACCGTAATTCAGAAGACTTGCTG 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232 AAAAATACGGTGGGCTATTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAGTTAAA 291
                                                                                                      -----AAAAACACAAATGGCCTGAA 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 ATCCTTGTCGAGGATGTAGACCTTCTGAAACTCTTCTACGCGTAAGCAACGGTTATACAGG
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                                              AAAAATTCCCGACGACTATTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAGTTAAA
                                                                                                                                                                                                                         CTCTCTGGTGGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAATCCCCGA
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                                                                                                                                                                                                                                                                                                                                                                     AATTTATTTGAAACTATTAACTTGGATGGACAAACTATTTTGATGGTAACCCATTC 608
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Pred. No. 4.4e-13;
0; Mismatches 259; Indels
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Sequence split into 22 fragments
Fragment Name Begin
ABN71527 00 1
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ABN71527 02
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ABN71527 20
ABN71527 21
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ABN71527_08
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sequence not defined in the specification, for amplifying a target sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence to substantial complementarily define the termini of the target sequence to be amplified, assay comprising contacting a test compound with the protein, and determining whether the test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus recting or preventing a disease or infection due to streptococcus media or ear infection. They are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful for identifying identified coding region from the genomic sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the properties of itendian or early of the printed on 27-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGAGCGTCCGGTTCAGGAAATCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACC 158
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Pred. No. 3.8e-14;
0; Mismatches 206; Indels
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Best Local Similarity 50.4
Matches 212, Conservative
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polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus pneumoniae.

Claim 1; Page 358-371; 1409pp; English.

Computer-readable medium with recorded Streptococcus pneumoniae

Fannon M;

Rosen CA, Barash SC,

Dillon PJ,

Choi GH,

Kunsch CA, C Dougherty BA;

WPI; 1998-272225/24.

(HUMA-) HUMAN GENOME SCI INC

97WO-US019588. 96US-0029960P.

30-OCT-1997; 31-OCT-1996;

17-MAY-1998

Streptococcus pneumoniae.

WO9818931-A2

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 219 ACGGTTATACAGGAAAATACGGTGGGCTATTTATTTCAAGATTATGCCTTGATTCCCCGA
                                                               CAGGACAGITAAATICAACCITCAGCITGCGGTGGAAAAAACACAAAATGGCCTGAAATICC
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The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (AAV52134 to AAV5254) recorded on it, or a representative fragment or a sequence at least 984 identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391. The nucleotide sequences depicted in SEQ ID NO:1 to 391 (AAV52134 to AAV52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences that hybridise to the target sequence and isolating the nucleic acid molecules trom the members, or (b) isolating make, DNA or cDNA produced from an organism, amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines

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15021 TGATGAAGGGAAATCTGGATTGATGGTGTTAATATTGCGGATTATAGTTCCCACCAGGG 15080
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Query Match
Best Local Similarity 50.4%; Pred. No. 2.2e-13;
Matches 212; Conservative 0; Mismatches 206; Indels 3;
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23-OCT-1998

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Sequence 21706 BP; 6489 A; 3946 C; 4879 G; 6392 T; 0 U; 0 Other;

tor S. pneumoniae

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides,
                                                                                                                                                                                                                                                                         Antibacterial; Listeria; food contamination; mutational analysis;
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                                                                                                                                                                                                                                      Listeria monocytogenes 4b contig DNA sequence #1015.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; SEQ ID NO 3886; 180pp; French
                                                                                                                                                                                                                                                                                                                            Listeria monocytogenes ATCC 19115
                                                                                RESULT 14
ABQ71073/c
ID ABQ71073 standard; DNA; 12278 BP.
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(first entry)
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29-AUG-2002
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                                  15261 Trichidaadadadadadadadagarcricarridadadagagagagagagaaaaaahidaaaahi 15320
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CTCTGGTGGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAATCCCCGAAT
                                                                                                   15321 TCTCCTTTGTGATGAACCGACTGGAGCCTTGGATTATCAGACGGGCAAGCAGGTTTTGAA
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Pred. No. 5.2e-13;
0; Mismatches 206; Indels
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Best Local Similarity 50.4'
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Continuation (15 of 22) on WP Sequence split into 22
WP Sequence split into 22
WP ABSS6454 00
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                       AACGAGATGGAATATCAGA-----CGAAAAAGAGGTTATGACTCTAAAAAAAAGAGGTG 9257
                                                                       9256 Tradgertrianariccaaaarrarceargargaaaargaaacaguduuragaaactra 9197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                       9196 TCCATTACAGGTGGGAAAAATCGCAAGCTGATGATAGAGCATTTAGAAGAAGTAGGAATG
GAGGATGTAGACCTTCTGAAACTCTCTACGCGTAAGCAACGGTTATACAGGAAAAATACG
                                                 GTGGGCTATTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAGTTAAATTCAACCTT
                                                                                                                                                361 CTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACAACT
                                                                                                                                                                        481 GCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCGACAAA
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Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prokaryotic essential gene; cell proliferation;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prokaryotic essential gene #21031
                                                                                                                                                                                                                                                                                                                                                                                                                                        ACA39374 standard; DNA; 1401 BP.
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Carr GJ,
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2001US-0342923P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Trawick JD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       design; gene
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25-OCT-2001;
08-FEB-2002;
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Wall D,
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The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an open required for proliferation or the activity of a gene in an open required for proliferation or that inhibits cellular proliferation; (8) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway confideration; (7) identifying a compound that inhibits product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling an encound sactivity; (11) a culture comprising strains in which the gene or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of an organism; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for cellular proliferation to isolate campings nucleic acids required for proliferation to isolate campings nucleic acids required for proliferation in cells other than S, sureus, S, typhimurium, confident and gene or P, aeruginosa. The present sequence is one of the target provestyrous confidence of the printed specification, but was obtained in cell corm to form part of the printed specification, but was obtained in cellular proliferation and provession of the print of the print of the print of the print of the print of the print of the print of the print of the print of the print of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCTTATTAATTTTTGGTGATGAACCTACTGGGGCACTTGATCTTGAGATGACCCAAATT 1224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 GGAGCGTCCGGTTCAGGAAAATCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160 AGTICCGGACAGAICCIIGICGAGGAIGIAGACCIICIGAAACICICACGCGIAAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     865 TCTAGTGGTAGTGTTATTGTCAATGGTTATAACATGATTTGTTTAAATGATAGAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 CGGTTATACAGGAAAAATACGGTGGGCTATTTATTTCAAGATTATGCCTTGATTCCCGAC
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Pred. No. 1e-13;
0; Mismatches 209; Indels 12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280 AGGACAGTTAAATTCAACCTTCAGCTTGCGGTGGAAAAAACAC---
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50.1%;
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Best Local Similarity
Matches 222; Conserv
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Sequence 36, Appli
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Sequence 2565, Ap
Sequence 1259, Ap
Sequence 2474, Ap
Sequence 2474, Ap
Sequence 72, Appl
Sequence 1758, Ap
Sequence 1758, Ap
Sequence 1758, Ap
Sequence 1758, Ap
Sequence 187, Appli
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Sequence 189, Ap
Sequence 2724, Ap
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Sequence 93, Appl
Sequence 1, Appli
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3: /cgn2_6/ptodata/2/ina/6A_COMB.seg:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seg:*
5: /cgn2_6/ptodata/2/ina/PCTUS COMB.seg:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-134-000C-1763

US-09-134-000C-2762

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Maximum Match 100%
Listing first 45 summaries
                                                           OM nucleic - nucleic search, using sw model
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## ALIGNMENTS

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GENERAL NEORATION:

APPLICANT: Charles Kunsch
ITIME OF INVENTION:
APPLICANT: Charles Kunsch
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APPLICANT: Charles Kunsch
ITIME OF INVENTION:
APPLICANT: Charles Kunsch
COUNTRY: USA
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US-06-545-528D-1/c
Sequence 1, Application US/08545528D
Patent No. 6537773
TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragments
Patent No. 6537773
TITLE OF INVENTION: Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576972 AAAATITCTTCCAĞĞAGAATITGTTĞTTATTCTTĞĞTAAATCTĞĞTAGTĞĞTAĞĞ
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                                     8730 ATCAGCATTGATGCACTTTTAGAAGCGGTTGGGATGGATAGTTTGCAAAAGAAGCTTCCT 78789
                                                                                                                                                            78790 AATGAATTGAGTGGTGGCGACACAGCAACGTGTTTCCATTGCAAGAGCTTTTGCTAAAAAC 78849
                                                                                                                                                                                                                                                                  78850 CCCTTATTAATTTTTGGTGATGAACCTACTAGGGCACTTGATCTTGAGATGACCCAAATT 78909
                                                                                                                                                                                                                 127 TTGCTCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATCCTTGTCGAGGAT 186
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                                                                                                        388 TITGAACTCTCTGGTGGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: PB193PI
CURRENT APPLICATION NUMBER: US/08/545,528D
PRIOR PILING DATE: 1995-10-19
PRIOR PLILOM DATE: 1995-06-07
PRIOR PILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/473,545
PRIOR RILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 1
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Best Local Similarity 50.14
Matches 216; Conservative
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APPLICANT: Fraser et al.
IIILE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment
Patent NO. 6537777
IIILE OF INVENTION: Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15321 TCTCCTTTGTGATGAACCGACTGGAGCCTTGGATTATCAGACGGGCAAGCAGGTTTTGAA 15380
                                                                                                                                                            15081 CACCAATTACCGTAGAAATGATGTGGGGTTTGTTTTTCAGTTTTATAATCTAGTTTCTAA 15140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15261 TTCTGGAGGGAGCAACAGCGAGTCTCCATTGCACGCGCGTAGCCAAAAATCCTAAAAT 15320
                                                 .5021 TGATGAAGGGGAAATCTGGATTGATGGTGTTAATATTGCGGATTATAGTTCCCACCAGCG 15080
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                                                                                                           278
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                                                                                                                                                                                                                                                                                                                                                                                                                                  396 CTCTGGTGGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAATCCCCCGAAT 455
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                                                                                                                                                                                                              279 CAGGACAGTIAAATTCAACCTTCAGCTTGCGGTGGAAAAACACAAATGGCCTGAAATTCC
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12.2%; Score 74.6; DB 4; Length 580073;
Best Local Similarity 50.1%; Pred. No. 2.6e-14;
Matches 222; Conservative 0; Mismatches 209; Indels 12; Gaps
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CURRENT APPLICATION NUMBER: US/08/545,528D
CURRENT FILING DATE: 1995-10-19
PRIOR APPLICATION NUMBER: US 08/488,018
PRIOR FILING DATE: 1995-06-07
PRIOR PELICATION NUMBER: US 08/473,545
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
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Patent No. 6537773
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CRGANISM: Mycoplasma genitalium
US-08-545-528D-1
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LENGTH: 580073
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Sequence 1259, Application US/09543681A

Patent No. 6605709

Patent No. 6605709

Patent No. 6605709

Patent No. 6605709

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILITILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR PIPLING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09
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Sequence 3565, Application US/09107532A
Patent NO. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 AAGTICCGGACAGATCCTTGICGAGGATGTAGACCTTCTGAAACTCTCTACGCGTAAGCA 218
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-010-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/ACENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      );
NAME/KEY: misc_feature
);
SEQUENCE DESCRIPTION: SEQ ID NO: 3565:
US-09-107-532A-3565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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MATION FOR SEQ ID NO: 3565:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 813 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                             576552 GCAGTTAATAT 576542
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GCTCTAGATTT 491
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                  US-09-107-532A-3565
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481
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Gaps

154

256 274 311

214

358 394 418 454 478 514 538

334

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137 GTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATCCTTGTCGAGGATGTAGACCTTC 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312 -----GGAAAAACACAAATGGCCTGAAA-----TTCCTCAAGTACTTCATGCTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335 ATAGTGGGTTÄÄCCCCÄÄÄAGAAGCCÄÄÄGATCGTGTCCACGÄÄGTTCTGACAAAÄTCG
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Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                     Length 681;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                        Score 69.6; DB 4; 1
Pred. No. 2.2e-14;
0; Mismatches 239;
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STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              539 AAGGCGCCACCGTTGTTGTTGCTACGCA 566
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                   CURRENT APPLICATION NUMBER: US/09/134,000C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/055,778 PRIOR FILING DATE: 1997-08-15 SUMBER OF SEQ ID NOS: 6812 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 96, Application US/08956171E Patent No. 6593114 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
                                                                                                                                                                                                                                                                                       ; ORGANISM: Enterococcus faecalis
US-09-134-000C-2474
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 49.4%;
Matches 251; Conservative
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COUNTRY: USA
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-08-956-171E-96
                                                                                                                                                                                                                    SEQ ID NO 2474
LENGTH: 681
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                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM:
                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                                                                                                                                       Sequence 1763, Application US/09134001C

Sequence 1763, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: NUCLE: NUCLE: US/09/134,001C

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/065,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674
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Pacent No. 6417156
GENERAL INFORMATION:
PAPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAATCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATCCT 176
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Pred. No. 6.5e-15;
0; Mismatches 213; Indels 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTTCAGCTTGCGGTGGAAAACACAAATGGCCTGAAATTCCTC--
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                                                                                                      505
                                                                             GATGAACCAACCGGAGCTCTAGATTTAACAAACA
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US-09-134-001C-1763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 49.6
Matches 227; Conservative
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US-09-134-000C-2474
                                                                                                                                                                                                                                 US-09-134-001C-1763
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Gary Breton et. al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 11050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 216; Indels
                               MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM MSDOS version 6.2 SOFTWARE: ASCII Text CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/956,171E FILING DATE: 20-Oct-1997 CLASSIFICATION: <UNKnown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cracaccrecindaricaaaacarcaaagecaricar 9819
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Pred. No. 3.4e-13;
                                                                                                                                                                               PRICR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 3, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGRNT INFORMATION:
NAME: Mark J. Hyman
REFERENCE/DOCKET NUMBER: 46,789
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 96:
US-08-956-171E-96
                                                                                                                                                                                                                                                                                                                                                                        (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 11050 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                          (301) 309-8439
                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 96: SEQUENCE CHARACTERISTICS:
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                 COMPUTER READABLE FORM
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Matches 226; Conservative
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US-09-489-039A-3320
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Sequence 3320, Application US/09489039A Patent No. 6610836 GENERAL INFORMATION:

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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS FILE REPERSENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 3320
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Sequence 2762, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Dowcete-Stamm et al

APPLICANT: Lynn Dowcete-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUMBER: US/09/134,000C

TITLE OF INVENTION: NUMBER: US/09/134,000C

CURRENT APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR APPLICATION NUMBER: US 60/055,778

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: Patentin version 3.1

SEQ ID NO 2762

LENGIH: 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.9%;
46.0%;
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Best Local Similarity 46.0
Matches 225; Conservative
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207 GCCATCATGGGTGAGTCTGGTTCTGGTAAATCAACTCTTCTCAATATTTCTAGCTATGTTG 266
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Sequence 72, Application US/08961527

Patent No. 6420135

GENERAL INFORMATION:
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
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                                                                                                                              341 AAGTACTTCATGCTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTG
                                                                                                                                                            AATACCTAAAAATTGTCGGTTTGGAAACAAAGGCCAAATCAAAAGTTACTGAACTTTCTG
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                                                                                             Gaps
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                                                               Length 720;
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Pred. No. 6.7e-12;
0; Mismatches 235; Indels
                                                               Score 66; DB 4; Length 720
Pred. No. 4.4e-13;
0; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette, 3.50 inch, 1. COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REPLECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 72:
SEQUENCE CHARACTERISTICS:
LENGTH: 14872 base pairs
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2762
                                                             Query Match
Best Local Similarity 55.8%;
Matches 126; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 49.1%;
Matches 244; Conservative (
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nucleic acid
EDNESS: double
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NAME: Brookes, A. Anders
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-08-961-527-72
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91 GCACTGACTGGAGCGTCCGGTTCAGGAAAATCGACTTTGGTCAACTGTTTGGCACACTT 150

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US-09-134-001C-1758
US-09-134-001C-1758
Sequence 1758, Application US/09134001C
Patent Vol. 6380370
GENERAL INFORMATION:
TITLE DE INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE DE INVENTION: DEPLERANDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE DE INVENTION: DEPLEMENTION SPACE OF PRIOR AND THERAPEUTICS
TITLE PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/065,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-10-14
SEQ ID NO 1758
LENGTH: 11-14
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GACAAACCAAGTTCCGGACAGATCCTTGTCGAGGATGTAGACCTTCTGAAACTCTTACG 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             567 GCCATCATCACAGAACCTGAAATTCTCCTTGCGGACGAGCCAACAGGAGCCCTTGATTCC 626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCGACAAAGGCGCCCACCGTT 552
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                                                              267 GATAAACCAAGTCGTGGTCAGGTTTACTTGAATGGAACTGACACCGCAACTATTAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                  447 ATAACGGAGATGATGAAGAAATTGGTGGTGACAGCTGAGAATCTGGGTATTAACCAATTG
                                                                                                                                                                                                                                              271 ATTCCCGACAGGACAGTTAAATTCAACCTTCAGCTTGCGGTGGAAAAACACAAATGGCCT
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                                                                                                                        83 irtitgaaagacatagatartcatattgatgaaggtgaarttattgctarcatgggtccgr
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Pred. No. 1.2e-12;
0; Mismatches 262; Indels 18
                                                                                                                                                                                                                                                                                                                                                                       331 GAAAT ---- TCCTCAAGTACTTCATGCTG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     687 CTCATGGTAACCCACTC 703
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Matches 250; Conservative
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494 GGGCAATTGTTAATGAGCCTGAATATTATTATTAGATGAGTCTTTATCGCCATTAGATT 553
374 GTAAGTCAGAAATTAAGCGTAAGGTTACTGAAGCACTTCAGTTGGTGAAATTAAGTGGTT 433
                                                                                                              371 TCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACGAACTGCGTTGGCCC
                                                                                                                                                                                                                                                                                                                                                                                              US-09-21-017B-187/c
US-09-221-017B-187, Application US/09221017B
Sequence 187, Application US/09221017B
Setent No. 6444709
GENERAL INFORMATION:
TITLE OF INVENTION:
TUTHE OF INVENTION: P. GINGIVALIS NUCLECTIDES AND USES THEREOF
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
                                                                                                                                                                                                                                                                                         491 TAACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACT 530
                                                                                                                                                                                                                                                                                                                                             554 TAAAATTACGAACTGAAATGCAATATTTATTGAGAGAACT 593
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FastSEQ for Windows Version 2.0b
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APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
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REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 2734
TELEPHONE: 650-813-5600
PELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRICE APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRICE APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRICE APPLICATION DATA:
APPLICATION NUMBER: PP2211
FILING DATE: 09-APR-1998
PRICE APPLICATION NUMBER: PC7AU98
PRICE APPLICATION NUMBER: PC7AU98
PRICE APPLICATION NUMBER: PC7AU98
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
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HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304-1018
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette

COMPITER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 706141
INPORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 4635 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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ORIGINAL SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 602, Application US/09134001C
Sequence 602, Application US/09134001C
Sequence 602, Application US/09134001C
GENERAL INFORMATION:
FAPFLICANT: Lynn Occette-Stamm et al
APPLICANT: Lynn Occette-Stamm et al
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR PILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 602
LENGTH: 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 TCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATCCTTGTCGAGGATGTAG 190
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                                                                                                                       ----AAAAACACAAATGGC 328
                                                                                                                                                                           323 TTTTAGAAAATGTAAGTATTCCGCTAATTTATAATGGTTTGAGTAATAAGCGAGAAAAA 382
                                                                                                                                                                                                                                     329 CTGAAATTCCTCAAGTACTTCATGCTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTTT 388
                                                                                                                                                                                                                                                                                383 GCAAAGTTTTAGACGGACTTCATGACGTCGACTTAAAAGGTAAAGAGAATCTCTTACCAA 442
                                                                                                                                                                                                                                                                                                                                                   389 TIGAACTCTCTGGTGGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAATC 448
                                                                                                                                                                                                                                                                                                                                                                                                          443 ATAAATTGTCAGGAGGGCAGCAACAACGTGTAGCTATTGCCCGGGCAATTATTAATGACC 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 TTAAAGATGTCAGTAAGGGCTTTGAAGATGTACAAATACTAAATGAAATTAATATTGATA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITIACCAGGAACAAIGACAGCACIGACIGGAGCGICCGGIICCAGGAAAAICGACITIGC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 ingaaccadderanninnanacachannaddreceneaddhorddaaaaacaacaann 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 taaaacrcatagcaggarrigaararcccgaragrggagaratrararaagaraaac 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 ACCTICTGAAACTCTTACGCGTAAGCAACGGTTATACAGGAAAAATACGGTGGGCTATT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 CTATTGGTAAATGCCACCGAATAAGCGTAAGGTAAATACTGTATTCCAAGACTATGCAT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 IGITICCACATTRAAATGTATICGACAATATIGCATAIGGTTTAAAATTAAAAAATTAA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 TGGAAAAACACAAATGGCCTGAAATTCCTCAAGTACTTCATGCTGTTGGTCTTGAGTCGT 370
         227 ACAGGAAAATACGGTGGGCTATTTATTTCAAGATTATGCCTTGATTCCCGACAGGACAG 286
                                                             263 Trcchahrchiacrchadchrrchichthrianarhthanhrchanarhachth 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              503 CTAAGTTTATTATTGCCGATGAACCTACTGGCGCTCTTGATTCGAAGACATCTCAAGATA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 TCAATGACCTCAAGAAATCTTTTGGCGTTCGGATCTTATGGCAAGGTCTCAGTCATAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            563 TTATGGAGCTTTTCGTAAACTGAACAAAAACAGAATACAACTATTATT 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.5%; Score 64; DB 4; Length 1149; Best Local Similarity 45.2%; Pred. No. 3e-12; Matches 235; Conservative 0; Mismatches 285; Indels
                                                                                                                       287 TTAAATTCAACCTTCAGCTTGCGGTGG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-602
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US-09-134-001C-602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3466640 TACTGCTGGCGACGAGCCCACCGGAAACCTCGACCGGAGACCAGTAGGGACATCATGG 3466581
                                                                                                                                                                                                                                                             1555
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                                                                                                                                                                   1674 TCAGCTCTCCGCAGGACAACAGCAGCGCGTGCTATCGCCCGTGCCGTGGTGGCCAATCC 1615
                                                                                                                                                                                                                     509
                                                                                                                                                                                                                                                                                                                                               449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTCTGGTGGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAATCCCCGGAA 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   515 AAGCATTGAGAGCACTCGCCGACAAGGCGCCACCGTTGTTGTTGCTACGCACTCGCCCC 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: CDC 1551
COTHER INFORMATION: "n" bases at various positions throughout the sequence JOTHER INFORMATION: represent a, t, c or g
                                                                                                                              390 TGAACTCTCTGGTGGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAATCC
                                                                                                                                                                                                                 1614 GAAGCTCATCCTCGCCGATGAACCCACGGTAACCTCGACTCCAAAAACGGAGCCGATGT
                                                                                                                                                                                                                                                                                                      510 CATAGAAGCATTGAGAGCACTCGCCGACAAAGGCGCCACCGTTGTTGCTACGCACTC
                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, Ohn C.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFRENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 4403765;
                                                                                       .
0
                                           Length 4635;
                                       Score 63.8; DB 4; Length 46:
Pred. No. 8.5e-12;
0; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62.6; DB 3; Length 4 Pred. No. 1.7e-09; 0; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    1494 CGAGCACGATGCACGTAGTCCCCCCCCATCATCT 1456
                                                                                                                                                                                                                                                                                                                                                                                           570 GCCCCTCTTCCGAGAATCAGCGGATACCATTATCAAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09103840A Patent No. 629428 GENERAL INFORMATION APPLICANT: FLEISCHMAN, ROBERT D. APPLICANT: WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3466520 ACATCGTCGACTC 3466508
                                       Query Match
Best Local Similarity 55.7%;
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 53.0%;
Matches 134; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
US-09-103-840A-2/c
US-09-221-017B-187
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Search completed: July 30, 2004, 14:16:21 Job time : 111 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

T/23. Filbb

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July 30, 2004, 13:27:50 ; Search time 506 Seconds (without alignments) 5901.210 Million cell updates/sec - nucleic search, using sw model OM nucleic Run on:

US-09-868-338-7\_COPY\_1117\_1725 609 Title: Perfect score: Sequence:

1 atgatagaaatcaatgacct.......60gataccattatcaaacta 609 Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

6445838 Total number of hits satisfying chosen parameters:

3222919 seqs, 2451570024 residues

Searched:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications NA:\*

| cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
| cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
| cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
| cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
| cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
| cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
| cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	Sequence 9. Appli	Segmence 2058 An	Segmence 9384. An	Segmence 36, Appl	Sequence 3886. An	Segmence 27244. A	Semience 13 April	Semience 13. Annl	Semience 13 April	Semience 1: Appli	Segmence 1 April	Segmence 34668 b	Segmente 3820 An	Sequence 30817, A
ΔΙ	16 US-10-398-221-9	16 US-10-398-221-2058	US-09-815-242-9384	US-10-158-844-36	US-10-398-221-3886	US-10-282-122A-27244	US-09-960-870-13	US-09-960-858-13	US-10-251-668-13	US-10-205-220-1	US-10-205-220-1	US-10-282-122A-34668	US-10-398-221-3820	US-10-282-122A-30817
	16		σ	13	16	13	10	10	13	15	15	13	16	13
% Query Match Length DB	684707	3011208	711	21706	12278	1401			31241	580073	580073		5312	684
% Query Match	13,3	13.3	12.7	12.4	12.3	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.1	12.0
Score	80.8	80.8	77.4	75.4	75	74.6	74.6	74.6	74.6	74.6	74.6	74.4	73.6	73.2
Result No.	г	0	m	4	Ω M	9	7	80	6	10	c 11	12	13	14

Seguence 956, App	44		32	7	123	e 12	m	96	96	603	238	10	Sequence 27896, A	24	37	72	68,	18	17	equence 6,	20	10	52	9592	9	e 239	2421	e 195	e 29,	n)
US-09-738-626-956	US-10-627	US-09-73	US-10-282		US-09-070-927A-1	US-10-307-294-12	US-10-307-294	US-08-781	US-10-32	US-09-815-242-6038	US-09-070-9	US-10-282-		US-10-282-	US-10-398-	US-10-158-	US-09-070-9	US-10-194-	US-10-398-	US-10-398-	6 US-10-398-221-2	6 US-10-398-221-1	15-242	15-242-959	US-10-398-221-3588	US-10-282-122A-2	US-09-974-300-2421	0-158-844-19	US-10-114-170-29	ń
σ	13	σ	13	16	თ	15	15	œ	13	σ	σ	13	13	13	16	13	σ	13	16		٦	-	σ		16		0	13	15	10
999	789	3309400	1062	319630	32768	630	7000	11050	11050	687	29729	1149	1398	726	2293	14872	8921	4635	732	25	3011208	8	816	816	3438	05	577	6693	11	741
11.9		11.9	11.8	11.7	11.4	11.3	11.3	11.2	11.2	11.2	10.8	10.8	10.7	10.7	10.7	10.7	10.6	10.5	10.4	10.3	10.3	10.3	10.2	10.2	10.2	10.1	10.1	10.0	10.0	10.0
72.4	72.4	72.4	71.6	71.2	9.69	68.6	68.6	68.4	68.4	68.2	99	9:59	65.2	65	65	ø		63.8	. 63.6	63	63	62.6	62.2	62.2	62	61.6	•	61		60.8
12	16	c 17	18	19	20	21	22	23	24	25	26	27	28	53	30	31	(*)	(*)	c 34	m	36	37	38	99	c 40	41	42	c 43	44	45

# ALIGNMENTS

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346005 ATGATTGAATTAGTTAATGTCAGTAAAAGATACAAGATAAATTGGATTTTGGAAAAAGTC 346064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATGATAGAAATCAATGACCTCAAGAAATCTTTTGGCGTTCGGATCTTATGGCAAGGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Gaps
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Best Local Similarity 47.2%; Pred. No. 5.3e-14;
Matches 284; Conservative 0; Mismatches 312; Indels 6;
US-10-398-221-9

| Sequence 9, Application US/10398221
| Publication No. US20040018514A1
| Publication No. US20040018514A1
| APPLICANT: WONST, Frederik
| APPLICANT: GLASER, Philippe
| TITLE OF INVENTION: Listeria innocua, genome and applications
| FILE REFERENCE: 344 702 - US
| CURRENT PRILIGE DATE: 2003-03-27
| PRIOR APPLICATION NUMBER: US/10/398,221
| CURRENT FILING DATE: 2003-03-27
| PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
| PRIOR APPLICATION NUMBER: FR 00/12 697
| PRIOR APPLICATION NUMBER: FR 00/12 697
| PRIOR PILING DATE: 2000-10-04
| PRIOR PILING DATE: 2001-10-04
| PRIOR PILING DATE: 2001-10-04
| PRIOR PILING DATE: 2001-10-04
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| BRIOR PILING DATE: 2001-10-04
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// OTHER INFORMATION: n can be any nucleotide: a, g, c or t/u
US-10-398-221-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Listeria innocua
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
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TILLE REFERENCE: ELITEA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

CURRENT FILING DATE: 2001-03-21

PRIOR PELICATION NUMBER: 60/11,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-11-27

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-12-22

PRIOR PELING DATE: 2000-12-22

PRIOR PELING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR PRIOR DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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346065 TCTCTTTCTATTGGAGCTGGCGAATTTATTGCAGTCGGCGAGAGTGGTAGTGGGAAG 346124
                                                                                                          346125 ACAACGCTGCTAAATGTTATCGGACACCTAGATTCAAAAGATAGTGGGCAAGTTATTATT 346184
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                                                                                                                                                                181 GAGGATGTAGACCTTCTGAAACTCTTACGCGTAAGCAACGGTTATACAGGAAAATACG 240
                                                                                                                                                                                                                                                                          361 CTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACAACT 420
                                                   121 TCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATCCTTGTC 180
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US-10-398-221-2058/C
Sequence 2058, Application US/10398221
Sequence 2058, Application US/10398221
Sequence 2058, Application No. US20040018514A1
GENERAL INFORMATION:
APPLICANT: KURST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REPERRENCE: 344 702 - US
CURRENT FILING DATE: 2003-03-27
FRICK REPERRENCE: 2003-03-27
FRICK PRILING DATE: 2001-10-044
FRICK PILING DATE: 2001-10-04
FRICK PILING DATE: 2001-10-04
FRICK PILING DATE: 2001-10-04
FRICK PILING DATE: 2001-10-04
FRICK PILING DATE: 2000-10-04
SEQ ID NOS: 4025
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 2058
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13.3%; Score 80.8; DB 16; Length 36
Best Local Similarity 47.2%; Pred. No. 1.2e-13;
Matches 284; Conservative 0; Mismatches 312; Indels
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US-10-398-221-2058
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121 TCGACTTTGCTCAACTGTCTTGGCACACTTGACAAACCAAGTTCCGGACAGATCCTTGTC 180
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APPLICANT: Trankck, John D.
APPLICANT: Trankck, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
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Publication No. U520040018514A1
GENERAL INFORMATION:
APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
TITLE OF INVENTION: Listeria innocua, genome and applications
FILE REFERENCE: 344 702 - US
CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT PILING DATE: 2003-03-27
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 4025
                                                                                                                                                                                                                                                                                                                                                                     Length 21706;
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Pred. No. 4.5e-13;
0; Mismatches 206;
FILING DATE: 1996-10-31
ATTORNEY/AGENT INFORMATION:
NAME: Hyman, Mark J.
REGISTRATION NUMBER: 46,789
ERFERENCE/DOCKET NUMBER: PB340P1D1
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                     TOPOLOGY: linear
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SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-158-844-36
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ORGANISM: Listeria monocytogenes 4b
FEATURE:
                                                                                                                                                                                   LENGTH: 21706 base pairs
                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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SEQ ID NO 3886
LENGTH: 12278
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50.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                         212; Conservative
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Best Local Similarity
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Sequence 36, Application US/10158844
Sequence 36, Application No. US20040029118A1
GENERAL INFORMATION:
APPLICANT: Kunsch et al.
TITLE OF INVENTION: Streptococcus pneumoniae Polymucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
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                                                                                                                                                                                                                                                                                                                      142 GCCAAGTCAACAGTTCTTAACCTTCTTGGGGGAATGGATACCAATGATGAAGGGGAAATC
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                                                                                                                                                                                                            Length 711;
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Pred. No. 1.4e-14;
0; Mismatches 226; Indels
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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/961,527
APPLICATION NUMBER: US 60/029,960
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APPLICATION NUMBER: US/10/158,844
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OPERATING SYSTEM: Windows
SOFTWARE: ASCII Text
                           TYPE: DNA ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                            Query Match
Best Local Similarity 50.8%;
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20850
COMPUTER READABLE FORM:
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                                                                                                                                  ... (711)
                                                                                                   ; NAME/KEY: CDS
; LOCATION: (1)...
US-09-815-242-9384
     LENGTH: 711
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                                                                             FEATURE:
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Sequence 13, Application US/09960870 Publication No. US20030134281A1 GENERAL INFORMATION:
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US-09-960-870-13
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                                                                                                                                                                                   1 ATGATAGAAATCAATGACCTCAAGAAATCTTTTGGCGTTCGGATCTTATGGCAAGGTCTC
                                                                                                                                             9
                                                                                                           Length 12278;
                                                                                                       Score 75; DB 16; Length 12
Pred. No. 4.4e-13;
0; Mismatches 316; Indels
; NAME/KEY: misc_feature
; LOCATION: (1)..(end)
; OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
US-10-398-221-3886
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                                                                                                     12.3%; 'nilarity 46.5%; 'Conservative 0;
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                           Similarity
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Pred. No. 1.7e-13;
0; Mismatches 209;
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PELING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-23
PRIOR PRING DATE: 2000-05-26
PRIOR PRING DATE: 2000-05-06
PRIOR PRING DATE: 2000-05-06
PRIOR PRING DATE: 2000-05-06
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-05-09
PRIOR PILING DATE: 2000-10-09
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PRIOR PILING DATE: 2000-11-27
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PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-10-29
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
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US-10-282-122A-27244
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milarity 50.1%;
Conservative 0
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Best Local Simi
Matches 222;
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                                                            8214 GGCCCTTCAGGATCTGGTAAACCÁCATTACTAAACATTATTTCAGGGATGGATAGAGCT 8273
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Sequence 13, Application US/10251668

Publication No. US20040063097A1

GENERAL INFORMATION:

APPLICANT: Brans, Glen

TITLE OF INVENTION: USE

TITLE OF INVENTION: USE

TITLE OF INVENTION: USE

TITLE OF INVENTION: USE

CURRENT APPLICATION NUMBER: US/10/251,668

CURRENT FILING DATE: 2002-09-20

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 13

LENGTH: 31241
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12.2%; Score 74.6; DB 13; Length
Best Local Similarity 50.1%; Pred. No. 1e-12;
Matches 222; Conservative 0; Mismatches 209; Indels
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, ORGANISM: M. genitalium
US-10-251-668-13
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US-10-251-668-13
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                                                                                                                                                                                                                                                                                                                                                   Score 74.6; DB 10; Length 3
Pred. No. 1e-12;
0; Mismatches 209; Indels
APPLICANT: Evans, Glen
TITLE OF INVENTION: USS
FILE REPERENCE: P-EA 4738
CURRENT APPLICATION NUMBER: US/09/960,870
CURRENT APPLICATION NUMBER: 2001-09-20
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FASESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 50.1%;
Matches 222; Conservative (
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; ORGANISM: M. genitalium
US-09-960-858-13
                                                                                                                                                                                                                                                    ; TYPE: DNA
; CRGANISM: M. genitalium
US-09-960-870-13
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Best Local Simil
Matches 222; C
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LENGTH: 31241
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US-09-960-858-13
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APPLICANT: Fraser et al.

APPLICANT: Fraser et al.

TITLE OF INVENTION: Nuclectide Sequence of the Mycoplasma Genitalium Genome, Fragments TITLE OF INVENTION: Thereof, and Uses Thereof
FITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB133F1D1
CURRENT APPLICATION NUMBER: US/10/205,220
CURRENT APPLICATION NUMBER: US 08/545,528
PRIOR APPLICATION NUMBER: US 08/488,018
PRIOR FILING DATE: 1995-10-19
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/473,545
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: PatentIn version 3.1
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Pred. No. 5.4e-12;
0; Mismatches 209;
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US-10-282-122A-34668
; Sequence 34668, Application US/10282122A
                                                                                                        GTCATAGAAGCATTGAGAGCACT 530
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; ORGANISM: Mycoplasma genitalium
US-10-205-220-1
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Best Local Similarity 50.1%;
Matches 216; Conservative C
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US-10-205-220-1/c
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TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment
TITLE OF INVENTION: Thereof, and Uses Thereof
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB133P101
CURRENT APPLICATION NUMBER: US/10/205,220
CURRENT FILING DATE: 1995-10-19
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
PRIOR FILING DATE: 1995-06-07
NUMBER: OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
SEQ ID NO: 1
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                                                                                                                                   8513
      3394 ITAACAGTTAGAGAAAACAITGAGATAGGAGCAAATCTTCAACCAGATCCTAGTAAAAGG 8453
                                                                                                                                                                                                                                           1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 1111 | 11
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                                                                                                                                                                                            388 ITTGAACTCTCTGGTGGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAAT
                                                                                                                                                                                                                                                                                                                         CCTGAAATTCCTCAAGTACTTCATGCTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3634 GİTTİAAAACAGİİTTINGCAAT 8656
                                                                                                                                                                                                                                                                                                                                                                                                                                                  508 GTCATAGAAGCATTGAGAGCACT 530
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Publication No. US20030170663A1
GENERAL INFORMATION:
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; ORGANISM: Mycoplasma genitalium
US-10-205-220-1
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1015 AGTGAAGGCAAATTATGGTAGATGGGCAGGATATTGCTCAATATAATGCAAAACAATTA 4074
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                                                 399 TGGTGGCGAACAACAACGAACTGCGTTGGCCCGGGTACTGCTCAAAAATCCCCGAATAAT 458
432 TGGCGGTCAGCAACAACGTACGGCGGCAGCCCGGGCATTCGTCCATAAACCAACAATTAT 491
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                                                                                                                                                                                                                                                                                                             Sequence 3820, Application US/10398221
| Publication No. US20040018514A1
| GENERAL INFORMATION:
| APPLICANT: KUNST, Frederik
| APPLICANT: GLASER, Philippe
| TILLE OF INVENTION: Listeria innocua, genome and applications
| FILE REFERENCE: 344 702 - US
| CURRENT PLILNG DATE: 2003-03-27
| FILE REPLICATION NUMBER: PCT/FR 01/03 061
| PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
| PRIOR FILING DATE: 2001-10-04
| PRIOR FILING DATE: 2001-10-04
| NUMBER OF SEQ ID NOS: 4025
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 5312;
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; OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
US-10-398-221-3820
                                                                                                                                                                                  492 TTTCGCAGATGAACCTACTGGCGCATTAGATTCTAAAA 529
                                                                                                                                                  459 TCTGGCTGATGAACCAACCGGAGCTCTAGATTTAACAA 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 73.6; DB 16;
Pred. No. 7.9e-13;
0; Mismatches 229;
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50.2%;
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Best Local Similarity 50.2
Matches 234; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 TAAAACGACTTTACTCAATGTGTTAAGTTCAATAGATACTATTTCAGGAGGAACTGTAGA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 TGTCGAGGATGTAGACCTTCTGAAACTCTCTACGCGTAAGCAACGGTTATACAGGAAAAA 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 ACATCTGGGTTTTATTTTTCAAGATTATAGCGTTTTACCCACATTAACAGTAAAAGAAAA 311
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INVENTION: Identification of Essential Genes in Microorganisms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 74.4; DB 13; Length 756; Pred. No. 1.4e-13;
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                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Identification of Esser
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Remaining Prior Application data removed NUMBER OF SEQ ID NOS: 78614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OR APPLICATION NUMBER: 60/267,931
OR PILING DATE: 2001-02-22
OR FILING DATE: 2001-02-09
OR APPLICATION NUMBER: 60/269,308
OR APPLICATION NUMBER: 60/269,308
APPLICATION DATE: 2001-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR APPLICATION NUMBER: 60/206, 848

OR APPLICATION NUMBER: 60/207, 727

OR PILING DATE: 2000-05-28

OR APPLICATION NUMBER: 60/207, 727

OR PILING DATE: 2000-09-08

OR PILING DATE: 2000-09-08

OR APPLICATION NUMBER: 60/230, 347

OR RELING DATE: 2000-09-09

OR APPLICATION NUMBER: 60/242, 578

OR PILING DATE: 2000-03

OR PILING DATE: 2000-03

OR PILING DATE: 2000-01-23

OR PILING DATE: 2000-01-23

OR PILING DATE: 2000-11-27

OR APPLICATION NUMBER: 60/25, 625

OR APPLICATION NUMBER: 60/25, 625

OR APPLICATION NUMBER: 60/25, 625

OR RILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Staphylococcus epidermidis
US-10-282-122A-34668
                                                    Hang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Syskind, Judith
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al Similarity 50.0%;
229; Conservative
                                                                                                                                                                                                    Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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242 TCGGTCTGGTCTTTCAGCAATTCCACTTAATCCCTTATTTAACTGCCTTGGAAAACGTCA 301
                                                                                                                                                                                                                302 Tellacacacaltalcacagiciaaticalgaagalgcagccaaggggggggggggagg 361
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                                                                                                                                                                                                                                                                                                                      353 CTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAAC
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11.9%; Score 72.4; DB 9;
Best Local Similarity 47.4%; Pred. No. 6e-13;
Matches 257; Conservative 0; Mismatches 276;
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APPLICANT: MAKAGAMA, SATOSHI
APPLICANT: ANDO, SEIKO
APPLICANT: ANDO, SEIKO
APPLICANT: OCHIAI, MIXIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: TATRISHI, NAOKO
APPLICANT: TATRISHI, NAOKO
APPLICANT: TATRISHI, NAOKO
APPLICANT: TERDA, MASATO
APPLICANT: TERDA, MASATO
APPLICANT: TERDA, MASATO
APPLICANT: TERDA, MASATO
APPLICANT: OZAKI, NAU
ARIOR OZAKI, NAU
APPLICANT: 1580-125
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR PELING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR PELING DATE: 2000-04-07
PRIOR PELING DATE: 2000-08-03
NUMBER OF SEQ. ID NOS: 7059
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APPLICANT: NAKAGAWA, SATOSHI
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Publication No.
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; ORGANISM: Cor
US-09-738-626-956
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SEQ ID NO 956
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFREENCE: ELITRA.038.

FILE REFREENCE: LITRA.038.

CURRENT APPLICATION NUMBER: 05/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/202,38

PRIOR FILING DATE: 2000-03-21

PRIOR PLING DATE: 2000-05-23

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-05-26

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-06

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/25,625

PRIOR PLING DATE: 2000-10-22

PRIOR APPLICATION NUMBER: 60/25,625

PRIOR APPLICATION NUMBER: 60/25,625

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING PAID APPLICATION NUMBER: 60/263,308

PRIOR FILING DATE: 2001-02-16

PRIOR FILING PAID APPLICATION NUMBER: 60/263,308

PRIOR FILING DATE: 2001-02-16
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12.0%; Score 73.2; DB 13; Length 684;
Best Local Similarity 46.4%; Pred. No. 3.3e-13;
Matches 283; Conservative 0; Mismatches 318; Indels 9
                                                                                                                                                                                        Sequence 30817, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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; ORGANISM: Pasteurella multocida
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Contact: Dr. Sergio Verjovski-Almeida
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               GenCore version 5.1.6
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CG954936
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Matches 215;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352 TCGACACTGTTGAACTGCCTTGGAACATTGGATCGTCCAACGGGTGAGCGTATCCTTTGG 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412 AATGGTAAAGATGTCGCTGCTGCAAGCGGTCGTCAGAGGCGACGGATGCGGAAATCTGAC 471
                                                                                                                Tel: +55-11-3091-2173
Fax: +55-11-3091-2186
Fax: +55-11-3091-2186
Fax: +55-11-3091-2186
Fax: +55-11-3091-2186
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                                                         SP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                         Instituto de Quimica - Universidade de Sao Paulo
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo
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Western X phytoplasma
Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
Acholeplasmatacees; Phytoplasma; 16SrIII (X-disease group)
1 (bases 1 to 622)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.3%; Score 75.2; DB 14; 53.8%; Pred. No. 2.4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Schistosoma mansoni"
/mol_type="mRXXX"
/db_xzef="taxon:6183"
/clone="Mil-0091T-L258-D10.B"
/sex="mixed pool"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="miracidium"
/clone_lib="ML1-0091"
/note="Vector: pGEM T-easy"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liefting, L.W. and Kirkpatrick, B.C.
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Departamento de Bioquimica
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Best Local Similarity 53.8
Matches 155; Conservative
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                                                                                             Brasil
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ORGANISM
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MEDLINE
PUBMED
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TITLE
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BH861070
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/note="Vector: pcosRW2; Site 1: SpeI; Pulsed-field gel purified DNA from Western X-disease phytoplasma was digested to completion with SpeI and cloned into the AvrII site of poosRW2. PoosRW2 was first modified by inscrting an annealed oligonucleotide containing the recognition sequences for AvrII, NCoI and MluI into the ECORI site."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CG954936 639 bp DNA linear GSS 15-DEC-2003
MBEBP10TF mth2 Medicago truncatula genomic clone 20820, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 516 ccgcacaitraitriaccccaicaaccaacaacciccaircaaaactgccaacaa 575
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Medicago truncatula
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 GGAGCGICCGGTTCAGGAAAATCGACTTTGCTCAACTGTCTTGGCACATTGACAAACCA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 GGAAAATCAGGATCGGCAAATCGACTCTTTAAACTTGTGGGAGGACTCGATAAGTGT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 gaccacrarriaakogocorrrrragicirrriarririccaacarrrraarrraaraaaga 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 angaangrirangaaaanarcgcrrragcraangagcrircagggccaaaaaaccggacaar 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 CCTGAAATTCCTCAAGTACTTCATGCTGTTGGTCTTGAGTCGTTCGAGGAAAAGCCAGTT 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    396 AAACTAATTTATAACTTATTAAAAAAAATGGAACTTTTAGGTTATGAAGAAAAAATT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGGACAGTIAAATTCAACCT-----TCAGCTTGCGGTGGAAAAACACAAAATGG 327
One Shields Ave, Davis, CA 95616, usa
Tel: 530 752 1697
Fax: 530 752 5674
Email: cwliefting@ucdavis.edu
Sequences were manually edited using Sequencher to remove vector
and low quality sequence.
Seq primer: Sp6
Class: cosmid ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 GATAGTGGAGATATTAATTAATTAAGTTTTCTATAAAAGAATTAAAACAAAATGATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 CGGTTATACAGGAAAATACGGTGGGCTATTTATTTCAAGATTATGCCTTGATTCCCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        160 AGTICCGGACAGATCCTTGTCGAGGATGTAGACCTTCTGAAACTCTTACGCGTAAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Western X-disease phytoplasma SpeI cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.4%; Score 63.4; DB 28; Length 622;
48.5%; Pred. No. 1.4e-08;
ative 0; Mismatches 216; Indels 12;
                                                                                                                                                                                                                                                                                                               /organism="Western X phytoplasma"
/mol type="genomic DNA"
/strain="Gensen"
/db xref="taxon:37704"
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Query Match
Best Local Similarity
Matches 115; Conserva
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Richins,R., Alvarado,K., Leger,J. and O'Connell,M.A. Richins,R., Alvarado,K., Leger,J. and O'Connell,M.A. Responsive transcripts in Phytophthora capsici-challenged roots of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 GGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACGA 417
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTCTTGATTCAATGGTAGGAGGTCATGGGACTCAACTTTCTGGTGGACAAAAGCAAAGA 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone lib="mth2"
/note="Vector: pBeloBAC11; Site 1: HindIII; Site 2: HindIII; Cook, D.R. and Kim, D.\overline{\mathbf{J}}, unpublished"
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0
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Pred. No. 3.3e-08;
0; Mismatches 88; Indels 0
                                                                                                                                                                                              9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2002)
Contact: O'Connell, MA
Department of Agronomy and Horticulture
New Mexico State University
MSC 30, P.O. Box 30003, Las Cruces, NM 88003, USA
Tel: 505 646 5172
                                                                           Town,C.D., Shetty,J., Koo,H. and Feldblyum,T.F. Sequencing of BAC ends from Medicago truncatula Unpublished (2003)
Cher_GSSs: MBEBP10TR
                                                                                                                                                                                                                                                                                                                              | . . 639
| /organism="Medicago truncatula"
| /mol_type="genomic DNA"
| /culfivat="genotype A17"
| /db_xref="taxon:3880"
| /clone="20820"
                                                                                                                                                                                                                                                     Email: cdtown@tigr.org
Seg primer: TGTAAAACGACGGCCAGT
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              538 AAAGGCGCCACCGITGITGITGC 560
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CA847456.1 GI:26997386
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Best Local Similarity 56.7%;
Matches 115; Conservative (
                                                                                                                                                           Contact: Chris Town
                                   Medicago.
1 (bases 1 to 639)
                                                                                                                                                                                                                   Tel: 301-838-3523
Fax: 301-838-0208
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Contact: Hyun S. Lillehoj
Animal Parasite Diseases Laboratory
Animal Parasite Diseases Laboratory
Animal and Natural Resources Institute, USDA
Animal and Natural Resources Institute, USDA
Baldy.104437, BARC-East, Beltsville, MD 20705, USA
Tel: 3015048771
Fax: 3015048771
Fax: 3015045103
Email: hlilleho@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trimmalt '-trim fasta. Vector identified
by cross match using options -minmatch 12 -minscore 12
Plate: 24 row. H column: 07
Seq primer: ATTAGGTACACTATAG
High quality sequence stop: 404.
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CD740366
ED740366.1 GI:32291215
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      282 AGTGCATTAGATGCAGAATCTGAGAGAGGTGGTACAAGAAGCATTGGATAGAATTATGATC 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallue.

1 (bases 1 to 404)

Min,W., Lillehoj,H.S., Ashwell,C.M., Matukumalli,L.K., van
Tassel,C. and Han,J.Y.

Chicken intestinal lymphocyte EST database as a resource for the unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                           'clone lib="CM334 Root cDNA"
'note="Organ: Root; Vector: Zap; Site_1: EcoR1; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           162 GGTCTAGACACCATGGTTGGAGATGGGACTCCACTTTCTGGTGGGCAAAAGCAAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                478 GGAGCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCGAC
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                                                                                                                                                                           /organism="Capsicum annuum"
/organism="Capsicum annuum"
/mol_type="mRNA"
/strain="Criollo de Morelos 334 (CM334)"
/db_xref="taxon:4072"
/db_xref="stage="folio"
/dev_stage="folio"
/dev_stage="folio"
/noculation"
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llarity 56.7%; Pred. No. 3.4e-08;
Conservative 0; Mismatches 88;
Fax: 505 646 6041
Email: moconnel@nmsu.edu
Seg primer: T3
High quality sequence stop: 668
Location/Qualifiers
1. .668
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Gallus gallus (chicken)
Gallus gallus
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/clore lib="lGAL - Chicken Intestinal Lymphocyte" | /clore | intestine, Vector: pGWY-SPORTE, Site_1: /note="forgan: Intestine, Vector: pGWY-SPORTE, Site_1: Sall; Site_2: Not!; Normalized library from chicken gut infected with coccidia duodenum and middle gut."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Frazer Murray
Dept. Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
Email: frazer.murray@bbsrc.ac.uk
/tissue_type="Gut"
/cell_type="Lymphocyte"
/dev_stage="Adult"
/lab_host="EMDH10B"
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Location/Qualifiers
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Gallus gallus
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ilarity 60.6%;
Conservative 0
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Matches 100; Conserv
                                                                                                                                                                                                                   Similarity
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4040991 1GAL - Chicken Intestinal Lymphocyte Gallus gallus cDNA
COOR 1GAL_38A17 5', mRNA sequence.
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Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim alt ' -trim fasta. Vector identified
by cross match using options -minmatch 12 -minscore 12
Plate: 38 row: A column: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 GGATTTGACACTGTAGTTGGAGAAAAAGGCATTCTACTTTCAGGTGGACAGAAAGCAGCGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 ATTGCAATTGCTCGGGCTCTGCTCAAGAATCCCAAAATTCTTCTGTTAGACGAAGCAACA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gailus (Baracoa, Chordata, Craniata, Vertebrata, Euteleostomi, Archosauria, Aves; Medonathae, Galliformes; Phasianidae, Phasianinae, Gallus.

I bases 1 to 542)

Min, W. Lillehol, H.S., Ashwell, C.M., Matukumalli, L.K., van Tassel, C. and Han, J.Y.

Chicken intestinal lymphocyte EST database as a resource for the Unpublished (2003)
                                                                                                                                                                                                      /clone lib="1GAL - Chicken Intestinal Lymphocyte"
/note="Organ: Intestine; Vector: pCMV-SPORT6; Site 1:
Sall; Site 2: Not1; Normalized library from chicken gut
infected with coccidia duodenum and middle gut."
                                                                                                                                                                                                                                                                                                                                                                                                              358 GGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACGA
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Hyun S. Lillehoj
Animal Parasite Diseases Laboratory
Animal and Natural Resources Institute, USDA
Bldg.1043, BARC-East, Beltsville, MD 20705, USA
Tel: 3015048771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Gallus gallus"
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/strain="white leghorn SC"
/db_xref="taxon:9031"
/clone="iGAL_38A17"
/sex="mixed"
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/db_xref="taxon:9031"
/clone="iGAL_24H07"
/sex="mixed"
      organism="Gallus gallus"
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/cell_type="Lymphocyte"
/dev_stage="Adult"
/lab_host="EMDH108"
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primer: ATTTAGGTGACACTATAG
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CD731492
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                                                                                     417
                                                                                                                                329
                                                                                                                                                                     /note="Vector: pBLUBSCRIPT SK; Site_1: BcoR1; Site_2: Xho1; Cloned unidirectionally. Primer: Oligo dT. Uni-ZAP XR vector. Average insert Size: 1.5kb.; 5' adaptor sequence: 5' GAATTCGGCACGAG 3'; 3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .619
/ Organism="Gallus gallus"
/ Mob_xref="taxon:9031"
/ Glone="ROS048607"
/ tissue_type="Tambryo"
/ dev_stage="Tambryo"
/ lab_host="Solk cells (kanamycin resistant)"
/ clone_lib="Stratagene Chick Embryo Lambda cDNA Library 937405]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1. (bases 1 to 619)
                                                                                         GGTCTTGAGTCGTTCGAGGAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACA
                                                                                                                                270 GGATTTGACACTGTAGTTGGAGAAAAAGGCATTCTACTTTCAGGTGGACAGAAGCAGGA
                                              Gaps
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0
    Length 542;
                                                                                                                                                                                                                                                               478 GGAGCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTG 522
                                                                                                                                                                                                                                                                                                        390 AGTGCTCTGGATGCTGAAATGAGTACCTAGTGCAAGAAGCTCTG 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.0%; Score 61; DB 9; Length 619; 60.6%; Pred. No. 7.9e-08; Live 0; Mismatches 65; Indels
                                              65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stratagene Chick Embryo Lambda cDNA Library Unpublished (2001)
Score 61; DB 14;
Pred. No. 7.5e-08;
0; Mismatches 65;
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/done liberCESECHN64"
//orde="Organ: whole embryo; Vector: pBluescript II KS(+);
Site_1: BCORI, Site_2: Not!; This normalized library was
constructed from I million independent clones. CDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand synthesis reaction.
Following this first strand synthesis reaction.
Goografic is a custom caction, double-stranded CDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Phasianinae; Gallus.
1 (Bases I to 798)
Boardman, P.B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Erown, W.R.A., Wilson, S.A. and Hubbard, S.J.
Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                               BU328328 1798 bp mRNA linear EST 28-NOV-2002
603496289F1 CSEQCHN64 Gallus gallus cDNA clone ChEST406a24 5', mRNA
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358 GGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACGA 417
                                                162 édatriréacacteradregadaaaaadecarretactrireaderégacadadede 221
                                                                                                          222 ATTGCAATTGCTCGAGCTCTGCTCAAGAATCCCAAAATTCTTCTGTTAGACGAAGCAACA 281
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University of Manchester Institute of Science and Technology
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                                                                                                                                                                                                                           478 GGAGCICTAGATTTAACAACAGTGAGCTAGTCATAGAAGCATTG 522
                                                                                                                                                                                                                                                                               282 AGTGCTCTGGATGCTGAAATGAGTACCTAGTGCAAGAAGCTCTG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .798
/organism="Gallus gallus"
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Mhite Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="ChEST406a24"
/tissue_type="whole embryo"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PO Box 88, Manchester, M60 1QD, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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BU328328
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//dev stage="adult"
/lab_host="DH10B"
//core=11b="CSEQCHNS8"
//core="Organ: small intestine; Vector: pBluescript II
//core="Organ: small intestine; Vector: pBluescript II
//site_1: BcoRI: Site_2: Not1; This normalized
library was constructed from 1 million independent clones.
cDNA synthesis was initiated using an oligo(dT) primer,
using methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
ECORI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1996): 791, except that a significantly longer
reannealing hybridization was used."
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1 (bases I to 743)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs
22235534
12445392
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BU399305 77-NOV-2002
603535206F1 CSEQCHN58 Gallus gallus cDNA clone ChEST49511 5', mRNA
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                           417
                                                                            176 GGATTTGACACTGTAGTTGGAGAAAAGGCATTCTACTTTCAGGTGGACAGAAGCAGCAG
                                                                                                                                      ATTGCAATTGCTCGAGGTCTGCTCAAGAATCCCAAAATTCTTGTTAGACGAAGCAACA 295
                        GGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACGA
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Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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                                                                                                                                                                                                                                                    478 GGAGCICTAGAITTAACAAACAGTGAGCTAGICATAGAAGCATTG 522
                                                                                                                                                                                                                                                                                                        296 AGTGCTCTGGATGCTGAAATGAGTACCTAGTGCAAGAAGCTCTG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Gallus gallus"

mol_type="mRNA"

/srxin="Compton Line 151"

db xref="taxon:9031"

/clone="ChEST49511"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PO BOX 88, Manchester, M60 1QD, UX Tel: 01612008930
Fax: 01612360409
Email: Simon. Hubbard@umist.ac.uk,
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
BU399305
BU399305.1 GI:25768361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (chicken)
Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="Female"
                                                                                                                                                                                             236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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AUTHORS
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BU399305
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/dev_stage="22"
/lab_host="DH10B"
/clone lib="CSEGHI14"
/note="Organ: head, Vector: pBluescript II KS(+); Site=1:
Roofs; Site=2: Not1; Modification of pBluescript II KS7+)
(Stratagene] Vector to accommodate cDNA produced with the
T-trimmed protocol (Construction of uni-directionally
cloned cDNA libraries from massenger RNA for improved 3'
end DNA sequencing by Glenn Fu, et al. U.S. Patent #
6,387,624). Cut pBluescript II KS(+) with NotI and EcoRI.
Ligate in double stranded adaptor containing BsgI and
BamHI sites [5'gagccggggagccggatccggatccgaaaaaaaag]
[5'aattcttttttcggatccggggctggacgc]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BU112595 907 bp mRNA linear EST 25-NOV-2002 603129071F1 CSEQCHL14 Gallus gallus clone ChEST102n17 5', mRNA
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                                                                                                                                                   222 ATTGCAATTGCTCGAGCTCTGCTCAAGAATCCCAAAATTCTTCTGTTAGACGAAGCAACA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Datary Variable Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi Archosauria; Aves; Neognathae, Galliformes; Phasianidae; Phasianinae; Gallus.

1 (Dases I to 907)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, Fong, W.T., Tickle, C., Brown, W.R., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                           GGTCTTGAGTCGATCGAGGAAAAGCCAGTTTTTGAACTCTCTGGTGGCGAACAACAACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 GGTCTTGAGTCGTTCGAGGAAAAGCCAGTTTTTGAACTCTTCTGGTGGCGAACAACAA
                                                                                     162 GGATTTGACACTGTAGTTGGAGAAAAAGGCATTCTACTTTCAGGTGGACAGAAGCAGCA
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University of Manchester Institute of Science and Technology
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60.6%; Pred. No. 9.4e-08;
iive .0; Mismatches 65;
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/mol_type="mRNA"
/strain="White Leghorn, Hisex"
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Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
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/clone="ChEST102n17"
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BU112595.1 GI:25316826
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Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simon Hubbard
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KEYWORDS
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Boardman, P.B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                452
453 AGTGCTCTGGATGCTGAAAATGAGTACCTAGTGCAAGAAGCTCTGGACCGGCTGATGGCA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae,
Phasianinae, Gallus.
                                                                                                                                                                                                                              478 GGAGCTCTAGATTTAACAAACAGTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCGAC
                                                                                                                                                         393 ATTGCAATTGCTCGAGCTCTGCTCAAGAATCCCAAAATTCTTCTGTTAGACGAAGCAACA
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Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
                                                                                                                                                                                                                                                                                                                                                            AAAGGCGCCACCGTTGTTGCTACGCACTCGCCCCTCTTCCGAGAAT 586
                                                                                                                                                                                                                                                                                                                                                                                                                       Aggeageacacritaarcarcecrcaccercrercracrarrcagaar 561
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/strain="White Leghorn, Hisex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PO Box 88, Manchester, M60 1QD, UK
121: 016.12008930
Fax: 016.12360409
Email: Simon.Hubbard@umist.ac.uk.
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/clone="ChEST375f3"
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/lab_host="DH10B"
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Gallus gallus
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BU407162
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Entartophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrartoideae; Oryzae; Oryza.

1 (bases 1 to 576)
85 Sasaki, T. and Yamanoto, K.
Rice cDNA from mature leaf (2000)
Unpublished (2000)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-6602, Japan
                                                                                                                                                                                                                                        AU090519 Fice mature leaf Oryza sativa (japonica cultivar-group) cDNA clone S20717, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H54613 358 bp mRNA linear EST 21-SEP-1995 yq92a09.rl Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE:203224 5' similar to SP:S21957 S21957 P-GLYCOPROTEIN PGP1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       417 AACTGCGTTGGCCCGGGTACTGCTCAAAATCCCCGAATAATTCTGGCTGATGAACCAAC 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             477 CGGAGCICTAGAITTAACAAACAGIGAGCTAGICATAGAAGCATIGAGAGCACTCGCCGA 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             246 AAGTGCACTTGATGTGGAGTCTGAGAGGTAGTTCAGGAGGCACTAAATAGAATGATGGT 305
                                                                   528 AGGCAGAGATACTGACAGCATTGAGGTCACTTGCCAATAACCGAACAGCAGTCTTTGTTG 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Emall: tssaaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT = RGP'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  357 IGGICTICAGICGTICGAGGAAAAGCCAGITITIGAACICTICGGIGGCGAACAACAACA
468 TGAAAGCTCCTCCTATTTTGCTGTGTGATGAAGCAACAAGTGCTCTGGATAGCACAACAG
                                       500 GTGAGCTAGTCATAGAAGCATTGAGAGCACTCGCCGACAAAGGCGCCCACCGTTGTTG
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9.8%; Score 59.4; DB 9; Length 5;
Best Local Similarity 55.6%; Pred. No. 2.5e-07;
Matches 114; Conservative 0; Mismatches 91; Indels
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/organism="Oryza sativa (japonic
/orltivar="Nipponbare"
/db_xref="taxon:39947"
/clone="$20717"
/tissue type="mature leaf"
/clone_lib="Rice mature leaf"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S37 CAAAGGCGCCACCGTTGTTGTTGCT 561.
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588 CT 589
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S Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J.,
Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y.,
Lai, Z., Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
L Unpublished (2002)
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu/
for details.
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                                                                                                                                                                                    BQ865169 759 bp mRNA linear BST 14-AUG-2002 QGC28024.yg.abl QG_ABCDI lettuce salinas Lactuca sativa cDNA clone QC2020024, mRNA sequence.
BQ865169 GI:22250634
                                                                                                                                                                                                                                                                                                    Lactuca sativa
Lactuca sativa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, campanulids, Asterales, Asteraceae, Cichorioideae,
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ATTGCAATTGCTCGAGGTCTGCTCAAGAATCCCAAAATTCTTCTGTTAGACGAAGCAACA 513
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                                                           478 GGAGCICTAGATITAACAAACAGTGAGCTAGTCATAGAAGCATTG 522
                                                                                         514 AGIGCTCIGGAIGCIGAAAAIGAGIACCIAGIGCAAGAAGCICIG 558
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Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 315
Source: IMAGE Consortium, Linn
This clone is available royalty-free through Lini; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: M13RP.
High quality sequence stop: 315.
High quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          426 bp mRNA linear EST 22-DEC-2000 mRNA sequence.
BF700602
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollnan,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soarses,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldman,P. and
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|db_xref="GDB:3772355"
|db_xref="taxon:9606"
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   ARABIDOPSIS ;, mRNA sequence.
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                                                                                                                                              Homo sapiens (human)
                                                                         H54613.1 GI:995139
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JOURNAL
COMMENT
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1 (Dases 1 to 426)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Preparation: TCC CLONETECH Laboratories, Inc.
cDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov h column: 20
Plate: LLCM1120 row: h column: 20
High quality sequence stop: 426.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratories (Palo Alto, CA)."
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/organism="Homo sapiens"
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BF700602.1 GI:11986010
                                               Homo sapiens (human)
                                                                            Homo sapiens
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

July 27, 2004, 16:28:59; Search time 54 Seconds (without alignments) 1062.169 Million cell updates/sec Run on:

US-09-868-338-9 1019 1 MIEINDLKKSFGVRILWQGL......VVVATHSPLFRESADTIIKL score: Sequence: Title: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database

A Geneseq 29Jano4:\*

1. geneseqp1980s:\*

2. geneseqp1990s:\*

4. geneseqp2001s:\*

5. geneseqp201s:\*

6. geneseqp203s:\*

7. geneseqp203bs:\*

8. geneseqp203bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		•			SUMMARIES		
Result		* Query					•
No.	Score	Match	Match Length	DB	TD .	Description	ion
н	1019	100.0	203	m	AAB12592	Aab12592	Brevibact
71	408		213	-	ABU01071	Abu01071	S. pneumo
٣	399	39.2	213		ABU02491	Abu02491	
4	399	39.2	213		ABP81472	Abp81472	Str
Ŋ	386	37.9	213	9	ABU00443	Abu00443	S. preumo
9	385	37.8	213		AAW80649	Aaw80649	s.
7	380.5	37.3	210		ABU02461	Abu02461	S. pneumo
80	380.5		210		ABP81469	Abp81469	Str
σ	373		211		ABB53309	Abb53309	Н
10	362.5		465		ABU36156	Abu36156	
11	3 5 5 6	35.2	258	·	AAU45701	Aau45701	
12	359		258		ABM42220	Abm42220	Propionib
13	353	34.6	270	7	ADC97592	Adc97592	E. faeciu
14	353	34.6	466		ABU35504	Abu35504	
15	352	34.5	237		ABP26089	Abp26089	Streptoco
16	348	34.2	250		ABP26471	Abp26471	ഗ
17	344.5	33.8	227		ABU39077	Abu39077	Protein e
18	344	33.8	207		ABB49925	Abb49925	Listeria
19	344		219		AAY34450	Aay34450	Porphorym
20	344	33.8	238		AAY34327	Aay34327	Porphorym
21	4	33.7	224		ABP26472	Abp26472	Streptoco
22	339.5	33.3	222	-	AAB76730	Aab76730	Corynebac
23		33.3	222	4	AAG90702	Aag90702	C glutami
24	m	33.3	259	S	50	Abb55099	Lactococc
25	m	33.3	648	4	AAU38402	Aau38402	Salmonell

		Aau37113 Staphyloc Aaw80648 S. pneumo Abb52924 Escherich			Abp65531 Bifidobac Adb12657 Alloiococ		
ABB47488 ABU16155	AEM / 2 / 84 AAU3 7 8 8 9 AAU3 4 1 4 6	AAU37113 AAW80648 ABB52924	ABB52958 ABB48879	ABU02123 ABU42928 ABP39755	ABP65531 ADB12657 ADB12655	ABB54027 AAU36276	ABP59941 ABU32430
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252	236	252 209 231	233	236 252 253	2000 3000 4000	668	663 241
33.2	33.0	33.0 32.7 32.7	32.7	32.7 32.6 32.6	322	3 2 5 2 2 5 3 2 5 5 5 4 5	32.4
338.5	999 939 939	336 333.5 333.5	333.5 333	3 3 3 3 3 3 3 3 3 3 3 3	331.5	331	330.5
27	0 0 0 0 0 7 0	332	3 3 4 5 5	9 B B	w 4 4	4 4 4 4 4 5 6	4 4 3

## ALIGNMENTS

Brevibacterium lactofermentum gltBD ORF2 protein SEQ ID NO:9. AAB12592 standard; protein; 203 AA. (revised)
(first entry) 12-SEP-2003 09-NOV-2000 AAB12592; RESULT 1 

Brevibacterium lactofermentum; ABC transporter; breeding; ATPase; corynebacterium; gltBD; L-glutamic acid.

Corynebacterium glutamicum,

WO200037647-A1.

29-JUN-2000.

99WO-JP007079. 16-DEC-1999;

98JP-00360621.

18-DEC-1998;

(AJIN ) AJINOMOTO CO INC.

Nakamatsu T; Matsui K, Kanno S, Kimura E,

WPI; 2000-452189/39. N-PSDB; AAA65395.

ABC transporter constituent of Brevibacterium lactofermentum, its encoded gene and variants, applicable in breeding Corynebacteria particularly for production of L-glutamic acid.

Claim 5; Page 30-31; 34pp; Japanese.

The present invention describes a protein (I) which can be used to construct an ATP binding cassette (ABC) transporter. ABC transporter DNAs can be used in breeding Corymebacteria particularly for production of L-glutamic acid. The present sequence represents an ORF (open reading frame) protein from the Brevibacterium lactofermentum gitbD gene, which is used in the exemplification of the present invention. (Updated on 12-SEP-2003 to standardise OS field)

Sequence 203 AA;

Query Match

Length 203; 100.0%; Score 1019; DB 3;

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27-MAR-2002; 2002WO-IB002163.
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(first entry)
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N-PSDB; ABX07781.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 213 AA;
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11-FEB-2003
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DDT 111-

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                                                                                                                                                                                                                                                                             or
                                                                                                                                                             EDVDLLKLSTRKORLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQVLHAVG 120
                                                                                                                                                                                                                                                  LESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEALRALADK 180
                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinflammatory; antibacterial; immunostimulant; auditory; respiratory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media cear infection.
                                                                                                                                                                                               BDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQVLHAVG
                                                                 1 MIEINDLKKSFGVRILMQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV
                                                                                              MIEINDLKKSFGVRILWQGLSHKFLPGTWTALTGASGSGKSTLLNCLGTLDKPSSGQ1LV
                        Gaps
                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S. pneumoniae type 4 strain protein from coding region #642
                        Indels
    Best Local Similarity 100.0%; Pred. No. 1.1e-103;
Matches 203; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus pneumoniae; type 4 strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 1284; 56pp; English.
                                                                                                                                                                                                                                                                                                                                               GATUVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                       ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABU01071 standard; protein; 213 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fraser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-MAR-2002; 2002WO-IB002163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAR-2001; 2001GB-00007658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene therapy; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-040579/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABX06354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-OCT-2003
11-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU01071;
                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                     121
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the target sequence, and where the parts of the primers having
cubstantial complementarity define the termini of the target sequence to
be amplified, assay comprising contacting a test compound with the
cube protein, and determining whether the test compound binds to the protein
and a Streptococcus pneumoniae bacterium, where one or more genes
cubering the proteins has been rendered inactive. The proteins, nucleic
acid molecules, antibody and compositions are useful as medicaments for
treating or preventing a disease or infection due to streptococcus
contacting or preventing a disease or infection due to streptococcus
contacting or preventing a disease or infection due to streptococcus
contacting or preventing a disease or infection due to streptococcus
contacting or preventing a disease or infection due to streptococcus
contacting or preventing a disease or infection for identifying contacting and antibitotics. The methods are useful for identifying
contacting and antibitotics. The present sequence is one of the 2469 proteins
contacting the identified coding regions from the genomic sequence
continued and for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
contacting the protein of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printed of the printe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 VLHAVGLESFE-EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DGTSLKDI---KPSVFFRDYLGYLFQDFGLIESQTVKENLNLGLVGKKLKEKEKISLMKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MIEINDLKKSFGVRILMQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Gaps

    pneumoniae type 4 strain protein from coding region #2069.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40.0%; Score 408; DB 6; Length 21
41.9%; Pred. No. 3e-36;
tive 44; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :|: |:|::||:|::|
178 LESLKNPNRTIIIATHNPLIWEQVDQVIRV 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae; type 4 strain.
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The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the special citication (available on a computer readable formath, or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the special strain genomic sequence appearing as ABS65454. Also included are an antibody which binds one of the proteins, treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the nucleic acid above or fragments between nucleicides 8-100 of a sequence contained within a Streptococcus nucleic acid sequence, where the first primer is substantially complementary to the target sequence of the interest is substantially complementary to the complement of the target sequence, and where the parts of the primers having substantially complementary to the complement of the target sequence or substantial complementarity define the terminio of the primers having comparising contacting a test compound with the protein, and determining whether the test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, antibody and compositions are useful for identifying a diagnostics and antibiotics. The methods are useful for identifying compared and acceptance of an antibody and compositions are useful for identifying compared sequence is one of the 2469 proteins secured. The sequence data for this patent diagnostic sand antibiotics. The methods are useful for identifying contacting or preventing or preventing or preventing or preventing or preventing or preventing or preventing or preventing or preventing or preventing or preventing or preventing or preventing or preventing or preventing or preventing or preventing or preventing or preventing or preventing or preventing or preventing or preven
                       New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
                                                                                                                                                                          Claim 1; SEQ ID NO 4138; 56pp; English.
                                                                                                                      ear infection
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61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQVLHAVG 120
                                                                                                                                                                                              -LESFE-----EKPVFELSGGEQORTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
                                                                                                                                                                                                                                                                 9
                                                                                                                         1 MIDIOGLEKKFNDRAIFSGENLKLEKGKVYALIGKSGSGKTTLLNILGKLEKIDGGRVLY 60
                                                                                                    1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV
                             Query Match 39.2%; Score 399; DB 6; Length 213;
Best Local Similarity 42.9%; Pred. No. 2.9e-35;
Matches 90; Conservative 40; Mismatches 70; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                  174 LRALADKGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                          Sequence 213 AA;
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Streptococcus pneumoniae; infection; otitis media; antibacterial;
                                                                                                          Streptococcus pneumoniae polypeptide SEQ ID NO 389.
                                                                          (first entry)
                                                                            04-MAR-2003
                                              ABP81472;
ABP81472
ID ABP
XX
AC ABP
XX
XX
DT 04-1
XX
XX
XX
XX
XX
XX
XX
XX
XX
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XX
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ABP81472 standard; protein; 213 AA.

RESULT

Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection;

S. pneumoniae type 4 strain protein from coding region #10.

(revised)
(first entry)

23-OCT-2003 11-FEB-2003

ABU00443;

Ą.

ABU00443 standard; protein; 213

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a Streptococcus pneumoniae genomic sequence, a fragment or degenerate variant of the polynuclectide or a nucleic acid sequence 95% identical to none of the polynuclectides. The S. pneumoniae polynuclectides and encoded polypeptides (ABPB1299-ABPB1674) are useful for treating or preventing S pneumoniae infections or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae. These are also useful for detecting S. pneumoniae in a biological sample or diagnosing S. pneumoniae in a biological sample or diagnosing S. pneumoniae infection in a subject. The polynucleotides have antibacterial activity and are useful in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQVLHAVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 -LESFE-----EKPVFELSGGEQORTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 ALEKVNLGYLDLEQKIYTLSGGEAQRVALAKTILKNPPLILADEPTAALDPENSEEVMNL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotides (ABZ72147-ABZ42522) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Gaps
                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                 New Streptococcus pneumoniae polynucleotides, useful for treating or preventing S. pneumoniae infections, or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae.
                                                                                                                                                                                                                                                              Russell DP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.2%; Score 399; DB 6; Length 213
42.9%; Pred. No. 2.9e-35;
iive 40; Mismatches 70; Indels
                                                                                                                                                                                                                                                              Chakravarti DN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 LRALADKGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 42; Page 642-643; 1091pp; English.
                                                                                                                                                                                                                                                                Green BA,
                                                                                                                                                                          2001US-0283948P.
2001US-0284443P.
                                                                                                                                        L2-APR-2002; 2002WO-US011524.
                                                                                                                                                                                                                            (AMCY ) AMERICAN CYANAMID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 42.9 es 90; Conservative
                                 Streptococcus pneumoniae.
diagnosis; gene therapy.
                                                                                                                                                                                                                                                              Zagursky RJ, Masi AW,
                                                                                                                                                                                                                                                                                                                     WPI; 2003-093010/08.
                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABZ42320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 213 AA;
                                                                   WO200283855-A2.
                                                                                                                                                                          16-APR-2001;
18-APR-2001;
                                                                                                     24-0CT-2002
                                                                                                                                                                                                                                                                                 Wooters JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches
#X8X#X#X#X##X##X###X###X###X
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antiinflammatory; antibacterial; immunostimulant; auditory; respiratory; gene therapy; vaccine.
                                                                                                                                                                New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media c
                       Streptococcus pneumoniae; type 4 strain.
                                                                                                                                                                                                       Claim 1; SEQ ID NO 20; 56pp; English.
                                                                                                                           Fraser C;
                                                                    27-MAR-2002; 2002WO-IB002163.
                                                                                    27-MAR-2001; 2001GB-00007658,
                                                                                                                           Masignani V, Tettelin H,
                                                                                                    (CHIR-) CHIRON SPA.
(GENO-) INST GENOMIC RES
                                                                                                                                          WPI; 2003-040579/03
                                                                                                                                                   N-PSDB; ABX05722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 213 AA;
                                      MO200277021-A2.
                                                      33-OCT-2002
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The invention relates to a protein comprising or having at least 50% identity to any of the 2469 amino acid sequences, identified in the specification (available on a computer readable formath, or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the specification (available on a computer readable formath, or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as ABS5654. Also included are an antibody which binds one of the proteins, Creating a patient by administering the protein. DNA or antibody (in a composition), a kit comprising first and second primers, which are the composition of the specification, for amplifying a target composition of the specification, for amplifying a target is substantial complementary to the complement of the target sequence, and where the parts of the primers having substantially complementary to the complement of the target sequence, and where the parts of the primers having substantially define the termining of the protein and determining whether the test compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes encoding the proteins has been rendered inactive. The proteins, nucleic acid molecules, and antibody and compositions are useful for identifying the proteins. The present sequence is one of the 2469 proteins expressed by the identified coding regions from the genomic sequence. Note: The sequence data for this patent did not form part of the printed sequence of the printed proteins. The present sequence is one of the 2469 proteins can fartive the sequence data for this patent did not form part of the printed sequence as fequence is one of the 2469 proteins. When the protein is the present sequence is one of the printed sequence.

Ä 61 FGQINLAVNSAKSQTIIREHISYLFQNFALIDDETVEYNIMLALKYVKLPKKDKLKKVVEE 120 EDVDLLKLSTRKORLYRKNTVGYLFQDYALIPDRTVKFNLQLAV-----EKHKWPEIPQ 114 1 MIBINDLKKSFGVRILWOGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60 9 6; Gaps 37.9%; Score 386; DB 6; Length 213; 40.2%; Pred. No. 7.9e-34; live 45; Mismatches 74; Indels Similarity 40.2% 84; Query Match Best Local 9 Matches g 8

61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAV-----EKHKWPEIPQ 114

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Streptococcus pneumoniae protein; recombinant; gene expression; DNA chip; virulence; antibody; infection; detection; treatment; hypothetical; cell wall biosynthetic, external target; minimal gene set protein.
115 VLHAVGLESFEEKPVFELSGGEQORTALARVLLKNPRIILADEPTGALDLTNSELVIEAL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a Streptococcus pneumoniae transport protein. The invention provides DNA sequences (AAV62201 to AAV63304) from the Streptococcus pneumoniae genome and corresponding protein sequences (AAW80605 to AAW80728). The protein sequences are classified as hypothetical, cell wall biosynthetic, external target, or minimal gene set proteins. A recombinant host containing a vector comprising any of the above nucleic acids can be used for the recombinant expression of the proteins. The invention also provides a DNA chip having arrayed on it at least 15 base pair fragment of any one or more of these DNA sequences. The DNA chip can be used methods for evaluating gene expression in S. pneumoniae and for identifying virulence genes in S. pneumoniae. Antibodies shat selectively bind to the above proteins or peptide fragments can be used to treat S. pneumoniae infection. The antibodies can also be used to detect S. pneumoniae cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae nucleic acid sequences - used in DNA chips for evaluating gene expression, and identification of virulence genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SR;
Skatrud PL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MIELKNITKTIGGKVILDNLSLRIDQGDLVAIVGKSGSGKSTLLNLLGLIDGDYSGRYEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dehoff BS, Hoskins JA, Jaskunas
Peery RB, Rockey PK, Rosteck PR,
J, Treadway PJ, Young Bellido ML;
                                                                                                                                                                              Treadway PJ,
                                                                                                                                      RALADKGATVVVATHSPLFRESADTIIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 236-237; 333pp; English.
                                                                                                                                                                                                                                                                                                                                                                               AAW80649 standard; protein; 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S. pneumoniae transport protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97WO-US022578.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96US-0036281P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burgett SG,
Norris FH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ELIL ) LILLY & CO ELI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-348529/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV65223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-DEC-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-DEC-1998
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Mills BJ,
Smith MC,
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The invention relates to a protein compurising or having at least 50% identified to any of the 2469 amino acid sequences, identified in the expecification (available on a computer readable format), or its fragment, expressed from 2469 of 2489 identified DNA coding regions from the expressed from 2469 of 2489 identified DNA coding regions from the Streptococcus pneumoniae type 4 strain genomic sequence appearing as Streptococcus pneumoniae type 4 strain genomic sequence appearing as treating a patient by administering the protein, DNA or antibody (in a composition), a kit comprising first and second primers, which are the composition), a kit comprising first and second primers, which are the sequence ontained within a Streptococcus nucleic acid sequence, the first primer is substantially complementary to the target sequence and the second primer is substantially complementary to the complement of the target sequence, and where the parts of the primers sequence to the target sequence, and where the parts of the primers sequence to substantial complementary to compound with the protein, and determining whether the test compound binds to the protein and a Streptococcus pneumoniae bacterium, where one or more genes concoming the proteins has been rendered inactive. The proteins nucleic acid molecules, antibody and compositions are useful as medicaments for treating or preventing a disease or infection due to streptococcus
New proteins and nucleic acid molecules from Streptococcus pneumoniae, useful as medicaments for treating or preventing a disease or infection due to streptococcus bacteria, such as pneumonia, sepsis, otitis media or
                                                      VLHAVGLESFEEKPVFELSGGEQORTALARVLLKNPRIILADEPTGALDLTNSELVIEAL 174
                                                                                Bacterial meningitis; pneumonia; sepsis; otitis media; ear infection; antiinfilammatory; antibacterial; immunostimulant; auditory; respiratory; gene therapy; vaccine.

    S. pneumoniae type 4 strain protein from coding region #2039.

                                                                                                                                     203
                                                                                                                                                       Streptococcus pneumoniae; type 4 strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 4078; 56pp; English.
                                                                                                                                   RALADKGATVVVATHSPLFRESADTIIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser C;
                                                                                                                                                                                                                                                                    ABU02461 standard; protein; 210 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-2001; 2001GB-00007658.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2002; 2002WO-IB002163
                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHIRON SPA.
INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                              (revised)
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                                                                                                                                                                                                                                                                                                                                          23-OCT-2003
11-FEB-2003
                                                                                                                                                                                                                                                                                                        ABU02461;
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            media or ear infection. They are also useful in developing vaccines, diagnostics and antibiotics. The methods are useful for identifying immunodominant proteins. The present sequence is one of the 2469 proteins expressed by the identified coding regions from the genomic sequence. Note: The sequence data for this patent did not form part of the printed aspecification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences. (Updated on 23-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                    114
                                                                                                                                                                                                                                                                                                                    60 RGKD---LANYKSSDFFRHELGYLFONFGLIENOSIEENLKLGLIGOKLSRSEORLROKO 116
                                                                                                                                                                                                                                                                                                                                                                                 117 ALBOVGLVYLDLDKRIFELSGGESQRVALAKIILKNPPFILADEPTASIDPATSQLIMEI 176
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 sepsis, otitis
                                                                                                                                                                                                                                                              1 MIEINDLKKSFGVRILMQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV
                                                                                                                                                                                                                                                                                                   61 EDVDLIKLSTRKORLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEI-----PQ
                                                                                                                                                                                                                                                                                                                                                              115 VLHAVGLESFE-EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated polynucleotides (ABZ72147-ABZ42522) a Streptococcus pneumoniae genomic sequence, a fragment or degenerate
                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for treating or diseases, e.g. pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae, infection, otitis media, antibacterial, diagnosis, gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Russell DP;
                                                                                                                                                                                                            11;
                                                                                                                                                                              Length 210;
 particularly S. pneumoniae, such as pneumonia,
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Streptococcus pneumoniae polynucleotides, useful preventing S. pneumoniae infections, or non-systemic otitis media, which are induced or exacerbated by S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pneumoniae polypeptide SEQ ID NO 386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chakravarti DN,
                                                                                                                                                                               DB 6;
                                                                                                                                                                                            ; Pred. No. 3.1e-33; 41; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                            174 LRALADKGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                               37.3%; Score 380.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP81469 standard; protein; 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-2001; 2001US-0283948P.
18-APR-2001; 2001US-028443P.
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                                                                                                                                                                                            41.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                            86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
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                                                                                                                                                                                              Similarity
                                                                                                                                                 Sequence 210 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABP81469;
                                                                                                                                                                              Query Match
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Matches
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ABP81469
ID ABP8
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variant of the polynucleotide or a nucleic acid sequence 95% identical to one of the polynucleotides. The S. pneumoniae polynucleotides and encoded polypeptides (ABP81299-ABP81674) are useful for treating or preventing S. pneumoniae infections or non-systemic diseases, e.g. otitis media, which are induced or exacerbated by S. pneumoniae. These are also useful for pneumoniae in a biological sample or disgnosing S. pneumoniae in a biological sample or disgnosing S. pneumoniae in the polynucleotides have antibacterial activity and are useful in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 RGKD---LANYKSSDFFRHELGYLFQNFGLIENGSIEENLKLGLIGQKLSRSEQRLRQKQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEI-----PQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 VLHAVGLESFE-EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MIEINDLKKSFGVRILWQGLSHKFLPGTWTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MIELKQVSKSFGERELFSNLSMTFEAGKVYALIGSSGSGKTTLMNMIGKLE-PYDGTIFY
                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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                                                                                                                                                                                                                                                                                                                                                         Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                              SD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :| | :::|||:|
LLSLRDDNRLIIIATHNPAIWEMADEVFTM 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRALADKGATVVVATHSPLFRESADTIIKL 203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sorokine A, Renault P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB53309 standard; protein; 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lactococcus lactis protein yabE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lactococcus lactis; IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                   Sequence 210 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FR2807446-A1
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16-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                86;
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Best Local 9
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                                                                                                                                                                                                                                                             174
                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
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     equivalent
                                                                                                                                                        1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV
                                                                                                                                                                                                                        EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAV-----EKHKWPEIPQ
                                                                                                                                                                                                                                                             115 VLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zyskind JW;
Xu HH;
                                           9
                                                                                                                                  Gaps
cheese. Note: The sequence data for this patent is based on equive patent WO200177334 (published 18-OCT-2001) which is available in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 standardise OS field)
                                                                                                                                 9
                                                                                                       Length 211;
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                                                                                                                                 Indels
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Forsyth |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein encoded by Prokaryotic essential gene #21683.
                                                                                            36.6%; Score 373; DB 5; Lo
39.2%; Pred. No. 2.1e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 64080; 1766pp; English.
                                                                                                                                                                                                                                                                                                                RALADKGATVVVATHSPLFRESADTIIKL 203
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                                                                                                                                                                                                                                                                                                                                                                                                         ABU36156 standard; protein; 465
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Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-00948993.
25-GCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002US-0362699P.
                                                                                                                      Local Similarity 39.2 tes 82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycoplasma pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zamudio C,
Trawick JD,
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                                                                                 Sequence 211 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-MAR-2002;
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                                                                                                                                                                                                                                                                                                                  175 ]
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                                                                                                          Query Match
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                                                                                                                         Best Loc
Matches
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encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) inhibiting cellular prolliferation or the activity of a gene in an operon required for prolliferation or the activity of a gene in an operon required for prolliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for prolliferation, or that inhibits cellular prolliferation; (8) identifying a gene required for cellular prolliferation of the biological pathway in which a prolliferation-required gene or its gene product lies; or a gene on which the test compound that inhibits prolliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound; a civity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the prolliferation of an organism. The antisense nucleic acids required in collular prolliferation of revening for homologous nucleic acids required for for cellular prolliferation of the screening candidate molecules for retional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the farmer prokarvotic essential genes. Note: The sequence data for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
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Sequence 465 AA;

IIBLKNVYKYITNGVTTNAVLKGIDLKLKAHDFIVILGPSGSGKTTLLNIISGMDRPSSG 290 57 QILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPE----I 112 113 POVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIE 172 351 DELLEAVGMKHLQKKLPNELSGGQQQRVSIARAFAKNPILIFGDEPTGALDLEMTQIVLK 410 1 MIEINDLKK--SFGV--RILWQGLSHKFLPGTMTALTGASGSGKSTLLLNCLGTLDKPSSG Gaps ص .. Length 465; ,9e-31; ... 70; Indels 35.6%; Score 362.5; DB 6; 36.7%; Pred. No. 9.9e-31; iive 54; Mismatches 70; 411 QFLAIKQRYKTTMVIVTHNNLIAQLADLVI 440 ALRALADK-GATVVVATHSPLFRESADTII 201 Ouery Match Best Local Similarity 36.7 Matches 77; Conservative 173 g 셤 엄 g ò ò à

AAU45701 standard; protein; 258 AA (first entry) 27-FEB-2002 AAU45701; RESULT 11 

Propionibacterium acnes immunogenic protein #6597.

SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant.

Propionibacterium acnes

WO200181581-A2

01-NOV-2001.

20-APR-2001; 2001WO-US012865.

Propionibacterium acnes transporter-related polypeptide #6896.

(first entry)

20-OCT-2003 ABM42220;

SEXEXEX

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ABM42220 standard, protein; 258

RESULT 12 ABM42220

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the treatment, prevention and diagnosis of medical conditions that treatment, prevention and diagnosis of medical conditions caused by publications, the discussion and diagnosis of medical conditions caused by practices. The discussed and osteonyalitis), uvoitis and endophthalmitis.

P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acceptance or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention only peptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and activity of P. acnes proteins and activity of P. acnes proteins and activity of P. acnes proteins and activity of P. acnes proteins also be used to therefore treat P. acnes infections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                     Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 SGQILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 V----LHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSEL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 GGSIVASGVSHNFSTTHNRNLVLDDVTVSMQPGVMTLLHGVSGSGKTTLLNIMSGLLKPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LPGTMTALTGASGSGKSTLLNCLGTLDKPS
                                                                                                                                                                                                                                                                     Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.2%; Score 359; DB 4; Length 258; 40.5%; Pred. No. 9.9e-31; tive 36; Mismatches 65; Indels 2
                                                                                                                                               Wang SS, Bhatia A;
                                                                                                                                             Mitcham JL, Wang Si
Jen S, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 VIEALRALA--DKGATVVVATHSPLFRESA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 VFELLRALAEDEKGRTVVLSSHDPTAKEYA 243
                                                                                                                                                                                                                                                                                                                                                           Claim 3; SEQ ID NO 6896; 1069pp; English.
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                 21-APR-2000; 2000US-0199047P.
02-JUN-2000; 2000US-0208841P.
07-JUL-2000; 2000US-0216747P.
                                                                                                                                             Persing DH, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                     treating acne vulgaris.
                                                                                                                                                                                                           WPI; 2001-616774/71.
                                                                                                       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
es 85; Conserv
                                                                                                                                                                     L'maisonneuve J,
                                                                                                                                                                                                                             N-PSDB; AASS9526
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                                                                                                                                               Skeiky YAW,
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154 VMAIEALERVGIAHLQDRYPRQLSGGEAQRVGIARAIAGDRPILLADEPTGQLDRRNSQM 213

170 VIEALRALA--DKGATVVVATHSPLFRESA 197

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antiseborrhoeic; dermatological; antibacterial;

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Acne vulgaris; antiseborrhoeic; dermatolog
immunostimulant; immune response; vaccine.
     Propionibacterium acnes.
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214 VFELLRALAEDEKGRIVVLSSHDPTAKEYA 243
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Matches 76; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-2003.
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                                                                                                                                                                     ADC97592;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polymuclectide (ACF64415-ACF64733)

encoding a Propionibacterium acnes protein. The invention also relates to polypeptides encoded by the polymuclectides (RAM35524-AAM64556) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a additionally encompasses expression vectors and host cells comprising a polypeptide of the invention; animune response specific for a p. acnes polymuclectides, dathbodies and immune response specific for a p. acnes polypeptide and an isolated T cell population comprising P acnes polypeptides, or intibodies, fusion proteins, T cell populations, or antigen-presenting cells that express the polypeptide); a method and kit for detecting or determining the presence or absence of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a patient; and a method for diagnosing, preventing or treating acne ploypeptides are useful for diagnosing, preventing or treating acnes confined acid hybridisation. The vaccine composition is useful for the sequence represents a specifically oliaimed polypeptide which is predicted to be encoded by an ORP (open reading frame) contained within the P. acnes polymucleotides of the invention, Note: The sequence data for this patent did not form part of the printed specifically polypeptide accompanied by the proper patient of the printed specifically polypeptide print place of the invention of the printed specifically polypeptide.

In electr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 V----LHAVGLESFEEKPVFELSGGEQORTALARVILKAVFRIILADEPTGALDLTNSEL 169
                                                                                                                                                                                                                                                                                                                                                                                                                           New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 SGQILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 SGTVFVEGSDIYSLSTSERDDIRLNRIGMIFQEHSLIVDFTVRENVELILRVRGFGSRSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 GVRILWQGLSHKF-------LPGTMTALTGASGSGKSTLLNCLGTLDKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34 GGSIVASGVSHNFSTTHNRNLVLDDVTVSMQPGVMTLLHGVSGSGKTTLLNIMSGLLKPT
                                                                                                                                                                                                                                                             Maisonneuve JL;
Jones R, Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 359; DB 6; Length 258; ; Pred. No. 9.9e-31; 36; Mismatches 65; Indels ;
                                                                                                                                                                                                                                                                Bhatia A,
Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3k; SEQ ID NO 6896; 1481pp; English.
                                                                                                                                                                                                                                                                Persing DH,
Lodes MJ,
                                                                                                                                                                                                                                                                Mitcham JL, Skeiky YAW, Persi
Zhang Y, Wang S, Jen S, Lode
Barth B, Vallieve-Douglass J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.2%;
                                                                                                                           11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                       15-OCT-2001; 2001US-00978825.
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Best Local Similarity
Local 85; Conserve
                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-381789/36.
N-PSDB; ACF64455.
                                                                                                                                                                                                                      (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 258 AA;
                                  WO2003033515-A1.
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The invention relates to an isolated mucleic acid derived from Enterococcus faecium encoding an Enterococcus faecium polypeptide having one of 10 fully defined sequences given in the (or comprising 40 composition) and the compression of the mucleic acids, its complement or sequences hybridising to it). Also included are a comprising the mucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid operably linked to transcription regulatory element, a cell comprising the vector and a single-stranded probe comprising the nucleic acid. The mucleic acids are chosen from 364 disclosed proteins. The nucleic acids is useful for Idagnosing pathological conditions regulting from E faecium bacterial infection (e.g. urinary tract infection) and for screening drugs such as agonists and antagonists. The nucleic acid is useful for recombinant production of Candida abloins nucleic acid is useful for recombinant production of Candida abloins and vaccines containing the nucleic acid are useful for preventing or treating Enterococcus faecium infections. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated nucleic acid derived from Enterococcus faecium encoding a
Enterococcus faecium polypeptide useful for detection, prevention and
treatment of a pathological condition resulting from a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                            Vaccine, urinary tract infection, bacteraemia, endocarditis, wound, abdominal-pelvic infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.6%; Score 353; DB 7; Length 27 clarity 40.9%; Pred. No. 4.9e-30; Conservative 36; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 7219; 243pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treating Enterococcus faecium infections. one if the disclosed E. faecium proteins.
                                                                                                                                                                                                                                            E. faecium protein sequence SEQ ID 7219.
ADC97592 standard; protein; 270 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0051571P.
98US-0085598P.
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                                                                                                                                                                   01-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-799836/75.
N-PSDB; ADC93938.
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The invention relates to an isolated mucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are:

10 a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway or proliferation, or that has an activity against a biological pathway or equired for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   screening
1 to
TVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIP-QVLHAVGLESFEEKPVFELSGGEQQ 138
                       197
                                                                                                    242
                                                                                                                                                                                                                                                                                                                                                                                          Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                   RTALARVLLKNPRIILADEPTGALDLTNSELVIBALR-ALADKGATVVVATHSPLFRESA
                                                                                   3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zyskind J
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                        encoded by Prokaryotic essential gene #21031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 25; SEQ ID NO 63428; 1766pp; English
                                                                                                                                                                                                                                                      Ä
                                                                                                                                                                                                                                                      standard; protein; 466
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ξί,
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06-SEP-2001, 2001US-00948993.
25-OCT-2001, 2001US-0342923P.
08-FEB-2002, 2002US-00072851.
06-MAR-2002, 2002US-0362699P.
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Carr G
                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                          Mycoplasma genitalium
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Trawick JD,
                                                                                                                                    DTIIKL 203
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DRVIHI 248
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                                123
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                                                                                                                                                                                                                                                      ABU35504
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Wall D,
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to which each of the strains is present in a culture or collection of braining to a strains; or (13) identifying the target of a compound that inhibits the prolliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular prolliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for prolliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in a lectronic format directly from NIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                      316 VGYIFQQYGLLPNLTVRENIEIGANLQPDPSKRISIDALLEAVGMDSLQKKLPNELSGGQ 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 QORTALARVLLKNPRIILADEPTGALDLTNSELVIEALRALADK-GATVVVATHSPLFRE 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Streptococcus protein for the treatment or prevention of infection or disease caused by Streptococcus bacteria, such as meningitis, and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                    21 SHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILVEDVDLLKLSTRKQRLYRKNT
                                                                                                                                                                                                                                                                                                                                                                                                  VGYLFODYALIPDRIVKFNLOLAVEKHKWP----EIPOVLHAVGLESFEEKPVFELSGGE
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                                                                                                                                                                                                                                                                                             10;
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                                                                                                                                                                                                                                                         34.6%; Score 353; DB 6; Length 466; 39.2%; Pred. No. 1.18-29; Live 42; Mismatches 61; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grandi G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Masignani V, Margarit Y RosI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptococcus polypeptide SEQ ID NO 1354.
                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABP26089 standard; protein; 237 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
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                                                                                                                                                                                                                                                                         Local Similarity 39.2 tes 73; Conservative
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(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus pyogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-352536/38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        196 SADTII 201
                                                                                                                                                                                                                            Sequence 466 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40200234771-A2.
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rettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                  81
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                                                                                                                                                                                                                                                           Query Match
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Matches
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The invention relates to a protein (ABP25413-ABP30895) from group B

creptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS

creptococcus progenes), comprising one of 5481 sequences (S1), given in

the specification. The proteins have antibacterial and antiinflammatory

creditorial to the proteins have antibacterial and antiinflammatory

creditorial to mucleic acids encoding (I), ABM$66044-ABN71526 and

creditorial to prevention of infection or disease caused by

Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes.

Nucleic acids encoding (I) are used to detect Streptococcus in a

composition comprising (I) or a nucleic acid encoding (I), may be

creditorial and antibactic composition. The disease caused by

creditorial to prevented or treated may be meningitis. Nucleic

creditorial to prevented or treated may be meningitis. Nucleic

acid encoding (I) may be used to recombinantly produce (I) and may be

creditorial therapy. Antibodies to (I) are used for affinity

chromatography, immunoassays, and distinguishing/identifying
detecting a compound that binds to the protein
                                                    Claim 1; Page 3291; 4525pp; English.
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Sequence 237 AA;

58 ILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIP-QVL 116 68 VIIDGXDIAHYTSKALTQYRRNAIGFVFQFYNLVPNLTAKENVELAVEIVADALDPVTIL 127 117 HAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPIGALDLTNSELVIEALRA 176 2 IBINDLKKSF--GVRILMQG--LSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQ 34.5%; Score 352; DB 5; Length 237; 38.3%; Pred. No. 5.2e-30; Live 45; Mismatches 76; Indels 177 LAD-KGATVVVATHSPLFRESADTII 201 Query Match
Best Local Similarity 38.33
Matches 79; Conservative 임 q ò à  $\stackrel{>}{\circ}$ 

Search completed: July 27, 2004, 16:35:05 Job time : 56 secs

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July 27, 2004, 16:34:05; Search time 19 Seconds (without alignments) 551.583 Million cell updates/sec
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1 MIEINDLKKSFGVRILWQGL.......VVVATHSPLFRESADTIIKL 203
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\* Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Match Length Result

Sequence 7219, Ap Sequence 4600, Ap Sequence 12101, A Sequence 12101, Ap Sequence 5411, Appl Sequence 5879, Ap Sequence 6167, Ap Sequence 13021, A Sequence 13021, A Sequence 6607, Ap Sequence 6607, Ap Sequence 6517, Ap Sequence 6517, Ap Sequence 6517, Ap Sequence 6517, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Sequence 5561, Ap Description US-09-107-532A-7219 US-09-134-001C-4600 US-09-252-991A-25336 US-09-134-00C-3925 US-09-543-681A-5411 US-09-134-00C-5617 US-09-134-00C-5617 US-09-134-00C-5617 US-09-134-00C-5617 US-09-134-00C-5617 US-09-134-00C-5617 US-09-134-00C-6517 US-09-134-00C-6517 US-09-134-00C-6517 US-09-134-00C-5561 US-09-134-00C-5561 US-09-134-00C-5518 US-09-134-00C-5518 US-09-134-00C-5518 US-09-134-00C-5518 US-09-134-00C-5518 US-09-134-00C-5518 US-09-134-00C-5518 US-09-134-00C-5518 US-09-134-00C-5518 US-09-134-00C-5518 US-09-134-00C-5518 US-09-134-000C-5469 US-09-252-991A-23361 US-09-107-533A-5335 US-08-919-573-2 US-08-919-573-4 332.53 330.53 322.54 322.55 322.53 305.5 306.5 3 

equence 6978 equence 6466 equence 1097	64, Ap 64, Ap 20657, 6078,	equence 3 equence 7 equence 5 equence 1 equence 1	Sequence 18, Appl Sequence 4327, Ap Sequence 4444, Ap Sequence 14256, A Sequence 72, Appl Sequence 74, Appl
09-107-532A- 09-543-681A- 09-489-039A-	09-305-984-64 09-493-940-64 09-252-991A-2 09-543-681A-6	US-09-134-001C-3731 US-09-543-681A-7794 US-09-107-532A-5226 US-09-305-984-18 US-09-073-541A-18	US-09-493-940-18 US-09-107-532A-4327 US-09-107-532A-4444 US-09-489-039A-14256 US-09-305-984-72 US-09-305-984-74
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### ALIGNMENTS

Sequence 7219, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street CITY: Waltham
STATE: Assachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: «Unknown>
COMPUTER: PC
OPERATING SYSTEM: US/09/107,532A
APPLICATION NATA:
APPLICATION DATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/081571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pemela Deneke
REGISTRATION NUMBER: 40,409
REFERENCE/DOCKET NUMBER: 40-007
TELEPHONE: (781)893-5007
TELEPHONE: (781)893-5007
TELEPAX: (781)893-5007
TELEPAX: (781)893-607
TELEPAX: (781)893-607
TELEPAX: 11 inear
NOCECULE TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: APPLICATION: YES.
ORIGINAL SOURCE:
ORIGINAL YES.
ORIGINAL SOURCE:
CONNETTER SOURCE:
CONNETTER TYPE: DIOCEGIN
CONTENTAL YES.
ORGANISM: Enterococcus faecium ;
NAME/KEY: misc\_feature
;
LOCATION: (B) LOCATION 1...270
;
SEQUENCE DESCRIPTION: SEQ ID NO: 7219:
US-09-107-532A-7219 RESULT 1 US-09-107-532A-7219

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396 LIBLRDIRKRYGGNGTPEVEVL-KGVSLSIHAGEFVAIVGASGSGKSTLMNILGCLDRPS 454
                                                                                                                                                                                                                                                                                                                                                                           SGQILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQL------AVEK 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 HKWPEIPQVLHAVGLESFEEKPVFELSGGEQORTALARVLLKNPRIILADEPTGALDLTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                         ch 32.4%; Score 330.5; DB 4
1 Similarity 37.3%; Pred. No. 7.9e-29;
81; Conservative 38; Mismatches 81
FILE REFERENCE: 107196.136
CURRENT APPLICATION WUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR APPLICATION WUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25336
LENGTH: 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 12101, Application US/09489039A
Patent No. 6610836
                                                                                                                                                                                             Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Klebsiella pneumoniae US-09-489-039A-12101
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35.0%;
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Best Local Similarity 35.0%
Matches 75; Conservative
                                                                                                                                                                                                                                                           Best Local Similarity
Matches 81; Conserv
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                                                                                                                                                                                                  ; ORGANISM: Pseudo:
US-09-252-991A-25336
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ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn Dougette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR PLING DATE: 1997-08-14 PRIOR PLING DATE: 1997-11-08 PRIOR PLING DATE: 1997-08-14 NUMBER: US 60/055,779 NUMBER OF SEQ ID NOS: 5674 SEQ ID NOS: 5674
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                              139 RIALARVLLKNPRIILADEPIGALDLINSELVIEALR-ALADKGATVVVATHSPLFRESA 197
                                                                                                                                                                                                                                                        TVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIP-QVLHAVGLESFEEKPVFELSGGEQQ 138
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                                                                                           LSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILVEDVDLLKLSTRKQRLYRKN
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                       Length 270;
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                                                          72; Indels
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37.6%; Pred. No. 6.3e-30;
tive 45; Mismatches 78;
                       Query Match
34.6%; Score 353; DB 4;
Best Local Similarity 40.9%; Pred. No. 2.6e-32;
Matches 76; Conservative 36; Mismatches 72
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AN
TITLE OF INVENTION: ABRUGINOSA FOR DIAG
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4600, Application US/09134001C Patent No. 6380370 GENERAL INFORMATION:
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US-09-252-991A-25336
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166

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Length 1049;

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GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PUBUMONIABE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709-2004001

CURRENT PEDLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR PELING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 12101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 GTYRVAGTDIAQLDGDALARLRREHFGFIFQRYHLLSHLTAAQNVEVPAVYAGNERRARL 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 PEIPQVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSEL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 ARAHELLVRLGLGERADYQPSQLSGGQQQRVSIARALMNGGEVILADEPTGALDSHSGEE 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MIBINDLXXXSF-----GVRILWQGLSHKFLPGTWTALTGASGSGKSTLLNCLGTLDKPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 LIELRDIRRSYPSGDGSVEVL-KGITLSIHAGEWVAIVGASGSGKSTLMNTLGCLDKPTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 329; DB 4; Length 672;
; Pred. No. 6e-29;
44; Mismatches 83; Indels
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                                                                                                           RESULT 5
US-09-134-000C-3925
; Sequence 3925, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: BUTEROCCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT FILING DATE: 1998-08-13
; PRIOR PILING DATE: 1998-08-13
; PRIOR PILING DATE: 1999-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PATENTIN VERSION 3.1
; SEQ ID NO 3925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58 ILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNL------QLAVEXHK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 ILLNGKNPNNLNQEQIAKFRRTELGFVFQSFNLMPTLTVBESNIILPLTLDGEKVSVMKRQ 128
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Patent No. 6342385

GENERAL INFORMATION:

TITLE OF INVENTION: MUTACIN I BIOSYNTHESIS GENES AND PROTEINS

PILE REPERENCE: UAB-17402/22

CURRENT APPLICATION WUMBER: US/09/627,376

CURRENT FILING DATE: 2001-05-30

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.0

SEQ ID NO 15

LENGTH: 246

TYPE: PRT

ORGANISM: Streptococcus mutans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 31.8%; Score 324; DB 4; Length 257; Best Local Similarity 35.1%; Pred. No. 5.3e-29; Matches 72; Conservative 52; Mismatches 65; Indels
209 VMAILHQLKAQGHTVIIVTHDPQVAAQAERIVEI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |: |: |: || || || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 || 100 |
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; ORGANISM: Enterococcus faecalis
US-09-134-000C-3925
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US-09-627-376-15
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Sequence 541, Application US/09543681A

| Sequence 541, Application US/09543681A
| Patent No. 665709
| GENERAL INFORMATION:
| APPLICANT: GRAY BRETON
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI)
| TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
| TITLE REPRENCE: 2709-1002-001
| CURRENT PAPLICATION NUMBER: US 60/128,706
| PRIOR PELING DATE: 1999-04-09
| NUMBER OF SEQ ID NOS: 8344
| SEQ ID NO 5411
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Patent No. 6617156
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: NUCLEIC ACID.
FILLE REPERBENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT PILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILLING DATE: 1997-08-15
PRIOR FILLING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patentin version 3.1
SEQ ID NO 6167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 SSCHIIFNNYQLEKVKDEEAAVFRSRHIGFIFQNFNLLNIFNNKDNLLIPVIISGSKVNS 120
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31.5%; Score 321; DB 4; Length 653;
Best Local Similarity 35.8%; Pred. No. 4.8e-28;
Matches 77; Conservative 46; Mismatches 78; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                              164 LINSELVIEALRALADKGATVVVATHSPLFRESADTII 201
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; ORGANISM: Proteus mirabilis
US-09-543-681A-5411
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US-09-543-681A-5411
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US-09-134-000C-6167
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us-09-868-338-9.rai

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62 DVDILKLSTRKORLYR-----KNTVGYLFQDYALIPDRTVKFNL-----QLAVEK 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107 -HKWPEIPQVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLT 165
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                                                                                                                                                                                                                                                                                                                                                                 Length 286;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 NSELVIEALRALADKGATVVVATHSPLF-RESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 LVNEVLAVMRELADEGRIMLIVIHEMRFAREVSSKVVFL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 30.1%; Score 306.5; DB 4; Best Local Similarity 36.5%; Pred. No. 6.2e-27; Matches 76; Conservative 40; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                      30.2%; Score 308; DB 4; 34.2%; Pred. No. 4.4e-27;
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US-09-134-001C-3832
; Sequence 3832, Application US/09134001C
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CURRENT FILING DATE: 2000-04-04 NUMBER OF SEQ ID NOS: 3840 ESQ ID NO 2931 LENGTH: 286
                                                                                                                                                                                                                                     ORGANISM: M.catarrhalis
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                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 75; Conserv
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US-09-489-039A-13021
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US-09-540-236-2931
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Sequence 2911, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION: District of the sequence of the sequence application of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of 
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CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 KAIAE--KYLKIVGLETKAKSKVTELSGGQQQRVAIARSLVNDPLLIMADEPTGALDSET 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107 HKWPEIPQVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTN 166
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                                                                                                                                                                                                                                                                                                                                                                          GQILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQL------AVEK 106
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                                                                                                                                                                                                                                                   LIBLRDINKFYPVGKEKLHVL-KELNITIHQGBFILIMGKSGSGKTTLMNIIGFLDRLTD 72
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                                                                                                    Gaps
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              Length 239;
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                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTEIMELLKELNEQGKTIVMVTHDEDMKKYASRVIHM 227
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                                                                                                    81;
         31.5%; Score 320.5; DB 4
35.9%; Pred. No. 1.2e-28;
ive 41; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5879, Application US/09134000C Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Enterococcus faecalis
US-09-134-000C-5879
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SOFTWARE: Patentin version 3.1
SEQ ID NO 5879
                                                                                                    Conservative
                                                    Similarity
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         Query Match
Best Local Simi
Matches 78;
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Sequence 13021, Application US/09489039A
Sequence 13021, Application US/09489039A
Betent No. 6610836
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US/09/489,039A
PRIOR RAPLICATION NUMBER: US 60/117,747
PRIOR PRILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 VLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEAL 174
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Sequence 6517, Application US/09134000C
Batent No. 6617156
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTIN VETSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 ILFKNED---IQNKGYSNHRKANISLVFQNYNLIDYLSPIENIRLVNKSAD----ESILF 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 AVGLESFE-EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEALRA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 ELGLDKKOIKRNVMKLSGGOOGNAIARALVSDAPIILADEPIGNLDSVTAGEIINILKT 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 30.0%; Score 305.5; DB 4; Best Local Similarity 37.5%; Pred. No. 5.8e-27; Matches 78; Conservative 45; Mismatches 72;
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1 Similarity 37.5%; Pred. No. 5.8e-27,
78; Conservative 45; Mismatches 72
                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...221
SEQUENCE DESCRIPTION: SEQ ID NO: 6667:
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                                                                                                                                                                                                                                                                                              ORGANISM: Enterococcus faecium
PELECOMMUNICATION INFORMATION
                                             INFORMATION FOR SEQ 1D NO: 6667:
SEQUENCE CHARACTERISTICS:
LENGTH: 221 amino acids
TYPE: amino acids
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                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 78; Conserva
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                                          APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: DEDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
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Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Acid AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQVLHAVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | : | : | : | : | : | : | | : | | : | | : | | EDNELTQHNVHLDNLRQK------PILLHKDS 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
30.0%; Score 306; DB 4; Length 242;
Best Local Similarity 33.5%; Pred. No. 5.8e-27;
Matches 73; Conservative 44; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:::| ||:: | EVVGDVLKVMRQLANESMTWVIVTHEMNFAKEISDKVV 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165 TNSELVIEALRALADKGATVVVATHSPLF-RESADTII 201
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APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/05171
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Waltham
STATE: Massachusetts
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                    GENERAL INFORMATION: APPLICANT: Lynn Dou
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RESULT 15
US-09-489-039A-10491
iS-09-489-039A-10491
j Sequence 1041, Application US/09489039A
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j Sequence 1041, Application US/09489039A
j Sequence 1041, Application US/09489039A
j GENERAL INCEMENTION:
i TITLE OF INVENTION:
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Query Match
29.7%; Score 303; DB 4; Length 396;
Best Local Similarity 35.3%; Pred. No. 2.7e-26;
Matches 73; Conservative 45; Mismatches 73; Indels 16; Gaps
                                                                                                                                                                                                                                                                                                177 LA-DKGATVVVATHSPLFRESADTIIKL 203
                                                                                 ПP
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Search completed: July 27, 2004, 16:37:19 Job time : 24 secs

1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60

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July 27, 2004, 16:36:31; Search time 45 Seconds (without alignments) 1412.673 Million cell updates/sec
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| cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1288442 seqs, 313154207 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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1019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                                                        Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		dę				
Result No.	Score	Query	Query Match Length DB	DB	ID	Description
	1 1 1 1 1 1 1 1			1		11 11 11 11 11 11 11 11 11 11 11 11 11
Н	399	39.2	213	16	US-10-474-776-389	Sequence 389, App
7	380.5	37.3	210	16	US-10-474-776-386	Sequence 386, App
ო	371.5	36.5	248	14	US-10-156-761-11171	11171
4	362.5	35.6	465	12	US-10-282-122A-64080	Sequence 64080, A
5	353	34.6		12	US-10-282-122A-63428	Sequence 63428, A
Q	344.5	33.8		12	US-10-282-122A-67001	Sequence 67001, A
7	339.5	33.3		σ	US-09-738-626-4456	Sequence 4456, Ap
80	339.5	33.3		12	US-10-627-476-442	Sequence 442, App
o,	339	33.3		σ	US-09-815-242-13995	Sequence 13995, A
10	337	33.1		12	US-10-282-122A-44079	Sequence 44079, A
11	336.5	33.0	315	14	US-10-156-761-12964	Sequence 12964, A
12	336	33.0		σ	US-09-815-242-13482	Sequence 13482, A
13	336	33.0	249	σ	US-09-815-242-5642	Sequence 5642, Ap
14	336	33.0	252	σ	US-09-815-242-12706	Sequence 12706, A
15	333.5	32.7	231	14	US-10-238-075-1256	Sequence 1256, Ap

7085 20,35 20,35 6035 6447 1493 11009 13827 105577	Sequence 15., Appl Sequence 13350, A Sequence 13690, A Sequence 1359, A Sequence 56938, A Sequence 56935, A Sequence 46319, A	Sequence 51603, A Sequence 11088, A Sequence 70607, A Sequence 6814, Ap Sequence 52619, A Sequence 52619, A Sequence 6966, A Sequence 10135, A Sequence 10135, A
US-10-28 US-09-815 US-10-284 US-10-284 US-10-286 US-10-286 US-10-286 US-09-815 US-09-815	10-282-122A-5012 10-815-242-13350 09-815-242-13350 00-815-242-13690 10-282-122A-7158 10-282-122A-7038 10-282-122A-6693	US-10-28 US-10-156 US-10-156 US-10-62 US-10-28 US-10-28 US-10-28 US-10-28
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116 117 118 118 119 119 119 119 119 119 119 119		
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### ALIGNMENTS

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Sequence 389, Application US/10474776
Publication No. US20040110181A1
Publication No. US20040110181A1
APPLICAMT: Wyeth
TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAE OPEN READING FRAMES ENCODING POLYPE
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
FILE REPERENCE: AM100649-PCT
CURRENT FILING DATE: 2003-10-14
NUMBER OF SEQ ID NOS: 752
SOFTWARE: Patentin version 3.1
SEQ ID NO 389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 -LESFE-----EKPVFELSGGEOORTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 ALEKVNLGYLDLEGKIYTLSGGEAQRVALAKTILKNPPLILADEPTAALDPENSEEVWNL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MIDIQGLEKKFNDRAIFSGLNLKLEKGKVYALIGKSGSGKTTLLNILGKLEKIDGGRVLY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 39.2%; Score 399; DB 16; Length 213; Best Local Similarity 42.9%; Pred. No. 3.3e-34; Matches 90; Conservative 40; Mismatches 70; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 LVDLKDENRIIIIATHNPLVWNKADEIIDM 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 LRALADKGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ; ORGANISM: Streptococcus pneumoniae US-10-474-776-389
US-10-474-776-389
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APPLICANT: Grant
APPLICANT: Grant
APPLICANT: Grant
APPLICANT: Vanamoto, Robert
APPLICANT: Vanamoto, Robert
APPLICANT: Porsyth, R.
APPLICANT: Xu, H.
TILLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPRENCE: ELITRA.034A
CURRENT FILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/201, 078
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
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PRIOR PILING DATE: 2001-02-09
                                                                                                                                         113 PQVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIE 172
                                                                                                                                                                                                                                                 57 QILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFN----LQLAVEKHKWPEI 112
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2 IBINDLKKSFG-----VRILMQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSG
                               9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1
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Best Local Similarity 36.7%; Pred. No. 8.1e-30;
Matches 77; Conservative 54; Mismatches 70; Indels 9;
                                                                                                                                                                                                                                                                                                                                                              173 ALRALAD-KGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 64080, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Trawick, John
Carr, Grant
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LENGTH: 465
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                                                                                              Sequence 386, Application US/10474776

Publication No. US20040110181A1

GENERAL INFORMATION:
APPLICANT: Wyeth
TITLE OF INVENTION: NOVEL STREPTOCOCCUS PNEUMONIAE OPEN READING FRAMES ENCODING POLYF
TITLE OF INVENTION: ANTIGENS AND USES THEREOF
FILE REFERENCE: AM100649-PCT
CURRENT APPLICATION NUMBER: US/10/474,776

CURRENT APPLICATION NUMBER: 2003-10-14
NUMBER OF SEQ ID NOS: 752
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 VLHAVGLESFE-EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.3%; Score 380.5; DB 16; Length 210;
41.0%; Pred. No. 3.1e-32;
tive 41; Mismatches 72; Indels 11; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 LRALADKGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHILBA, HIROSHI
APPLICANT: SHILBA, HIROSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
PRIOR FILING DATE: 2001-06-07
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Sequence 11171, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-10-474-776-386
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Best Local Similarity 41.0*
Matches 86; Conservative
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LENGTH: 248
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Best Local S
Matches 87
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APPLICANT: Carr, Garant
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: AV, H.
ITIE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITAA.034A
CURRENT APPLICATION NUMBER: 06/101,078
PRIOR APPLICATION NUMBER: 60/101,078
PRIOR PELING DATE: 2000-03-23
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,337
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-01-23
PRIOR PELING DATE: 2000-01-23
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
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PRIOR PELING DATE: 2000-11-27
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PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2001-02-09
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PRIOR PELING DATE: 2001-02-06
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PRIOR PELING DATE: 2001-02-06
PRIOR PELING DATE: 2001-02
                                                                 316 VGYIFQQYGLLPNLTVRENIEIGANLQPDPSKRISIDALLEAVGMDSLQXKLPNELSGGQ 375
                                                                                                                                                  137 OORTALARVLIKNPRIILADEPIGALDLINSELVIEALRALADK-GATVVVATHSPLFRE 195
                                                                                                                                                                                              VGYLFQDYALIPDRTVKFNLQLAVEKHKWP----EIPQVLHAVGLESFEEKPVFELSGGE 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 67001, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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; ORGANISM: Pasteurella multocida
US-10-282-122A-67001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Ohlsen, Kari
APPLICANT: Chisen, Vari
APPLICANT: Yskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
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436 LADLVI 441
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Best Local Similarity
Matches 83; Conserv
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TITLE OF INVENTION: Identification of Essential Genes in Microcganisms
FILE REPERSNCE: ELITRA.034
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/2030,335
PRIOR PILING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-06
PRIOR PELING DATE: 2000-09-09
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2001-12-22
PRIOR PELING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-16
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PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-02-17
PRIOR PILING DATE: 2001-02-18
PRIOR PILING DATE: 2001-02-18
PRIOR PILING DATE: 2001-02-18
PRIOR PILING 
                                                                                                                                  113 POVLHAVGLESPEEKPVFELSGGEQORTALARVLLKNPRIILADEPTGALDLTNSELVIE 172
                                                                                                                                                                                                                                                                            57 QILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPE----1 112
    231 IIELKNVYKYITNGVTTNAVLKGIDLKLKAHDFIVILGPSGSGKTTLLNIISGMDRPSSG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 SHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILVEDVDLLKLSTRKQRLYRKNT 80
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34.6%; Score 353; DB 12; Length 466;
Best Local Similarity 39.2%; Pred. No. 8.5e-29;
Matches 73; Conservative 42; Mismatches 61; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                      411 QFLAIKQRYKTTMVIVTHNNLIAQLADLVI 440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Oblisen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Wall, Daniel
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Trawick,
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US-10-282-122A-63428
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TITLE OF INVENT
FILE REFERENCE:
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Query Match
Best Local Similarity
Matches 80; Conserv
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ORGANISM:
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                                                             57 QILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVE---KHKWPEIP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .14 QVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
                                     118 AVGL-ESFEEKPVFELSGGEQORTALARŲLLKNPRIILADEPTGALDLTNSELVIEALRA 176
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38.1%; Pred. No. 8.3e-28;
tive 38; Mismatches 83;
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                                                                                                                                                                                                                                                                                                             APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGURII, HIROSHI
APPLICANT: MIZOGURII, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: SENOH, ARUHIRO
APPLICANT: SENOH, MASHO
APPLICANT: IKEDA, MASHO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT APPLICATION NUMBER: 200-12-18
                                                                                                                                          177 LADKGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
                                                                                                                                                                                                                                                    Sequence 4456, Application US/09738626
Publication No. US20020197605Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 442, Application US/10627476 Publication No. US20040030116A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Pompejus, Mark
APPLICANT: Kroger, Burkhard
APPLICANT: Schoder, Hartwig
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Best Local Similarity
Matches 80; Conserv
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LENGTH: 222
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63 VIANGQELNKLNQKALAKFRKESLGFIFQDYSILPTLTVKENIMLPLSVQKMSKATMEEN 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 ILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQ--- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 ---VLHAVGLESFEEKPVFELSGGEQORTALARVLLKOPRIILADEPTGALDLTNSELVI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MIBINDLKKSFGVRILWQGL---SHKFLPGTWTALTGASGSGKSTLLNCLGTLDKPSSGQ 57
PRIOR FILING DATE: 2000-09-06

PRIOR PLICATION NUMBER: 60/230,347

PRIOR PLING DATE: 2000-09-09

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-12-29

PRIOR FILING DATE: 2000-12-29

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-06

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

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PRIOR PLING DATE: 2000-01-02-09

PRIOR PLING DATE: 2000-01-02-09

PRIOR PLING DATE: 2000-01-02-02-09

PRIOR PLING DATE: 2000-01-02-02-03

PRIOR PLING DAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 BALRALADK-GATVVVATHSPLFRESADTIIKL 203
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APPLICANT: HORIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYCSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASAHIRA
TILLE OF INVENTION: NOVEL POLYNUCIEOTIDES
FILE REPERBNGE: 249-26
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT APPLICATION NUMBER: US/2001-204089
PRIOR FLING DATE: 2001-05-30
PRIOR FLING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 12264
ELENGTH: 215
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Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATCSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-12964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Staphylococcus aureus US-10-282-122A-44079
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Best Local Similarity 37.7%
Matches 80; Conservative
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APPLICANT: Forsyth, R.
APPLICANT: Porsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFRENCE: ELITRA.018
FILER REFRENCE: ELITRA.018
CURRENT APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MIEINDLKKSF-----GVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
33.3%; Score 339; DB 9; Length 648;
Best Local Similarity 36.9%; Pred. No. 4.3e-27;
Matches 79; Conservative 42; Mismatches 81; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 VIEALRALADKGATVVVATHSPLFRESADTIIKL 203
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CURRENT FILING DATE: 2001-03-21
PRIOR PLILING DATE: 2001-03-21
PRIOR PLILING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-03-21
PRIOR PLILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-05-26
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PRIOR PLILING DATE: 2000-12-27
PRIOR PLILING DATE: 2000-12-26
PRIOR FILING DATE: 2001-12-26
PRIOR FILING DATE: 2010-12-16
NUMBER OF SEQ ID NOS: 14110
SOPTWARE: PASISEQ for Windows Version 4.0
SOD ID NO 13995
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Xu, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -10-282-122A-44079
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Gaps

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4
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33.0%; Score 336.5; DB 14; Length 315; 37.7%; Pred. No. 2.8e-27; tive 39; Mismatches 82; Indels 11;
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199 TIIKL 203
                                         210 RVIQM 214
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US-09-815-242-12706
                                                                                                                                            US-09-815-242-5642
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SEQ ID NO 5642
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                                                                                                                                                                                                                     190 AEVLAQVGLQDKGRRRPGQLSGGQQQRVAIARALUTRPDVVFADEPTGALDTTTAAEILG 249
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                            130 TVHLGGTDITGLSENKLTALRRSRLGFVFQAFNLLPSLTVEQNVVLPLRLAGHRPDRRRA 189
                                                                                                                                                                                        113 PQVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 DYALIPDRIVKFNLQLAVEKHKWPEI-----PQVLHAVGLESFEEKPVFELSGGEQQR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 TALARVILKNPRIILADEPIGALDLINSELVIEALRALA-DKGATVVVATHSPLFRESAD 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 GELVIILGASGAGKSTVLNLLGGMDTNDEGEIWIDGVNIADYSSHQRTNYRRNDVGFVFQ 95
2 IEINDLKKSFG----VRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27 GIMTALIGASGSGKSTLLNCLGTLDKPSSGQILVEDVDLLKLSTRKQRLYRKNTVGYLFQ 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 33.0%; Score 336; DB 9; Length 236;
Best Local Similarity 40.5%; Pred. No. 2.1e-27;
Matches 75; Conservative 38; Mismatches 58; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, Howard

TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryoes
TITLE OF INVENTION: PROKARYOES

CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/205,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-01-23
PRIOR FILING DATE: 2000-01-23
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                     173 ALRALAD-KGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                  250 LLRQAVDVHGATVVMVTHDPTAAAWADRVLFL 281
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13482, Application US/09815242
Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT; CRGANISM: Streptococcus pneumoniae US-09-815-242-13482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Haselbeck, Robert
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71 GTDAAALDEEGRRRFRAEKIGLVFQQFHLIPFLTALENIMLAQHYHSVVDEAAARKVLEQ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                     62 DVDLLKLSTRKORLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPE---IPQVLHA 118
                                                                                                                                                                                                                                                                                                                                                                                                       119 VGLESFEEKPVFELSGGEQQRTALARVILKNPRIJLADEPTGALDLTNSELVIEALRALA 178
                                                                                                                                                                                                                                  2 IEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILVE 61
                                                                                                                                                       Gaps
                                                                                                                                                    ë.
                                                                                                 Length 231;
                                                                                              Query Match 32.7%; Score 333.5; DB 14; Length Best Local Similarity 38.0%; Pred. No. 3.8e-27; Matches 78; Conservative 32; Mismatches 92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 ROGRIIVMVTHNPALGQFADRILRL 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 DKGATVVVATHSPLFRESADTIIKL 203
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                        , ORGANISM: Escherichia coli
US-10-238-075-1256
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APPLICANT: Chleen, Kari I.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Xu, H. Howard
ITILE OF INVENTION: Prokaryotes
ITILE OF INVENTION: Prokaryotes
ITILE OF INVENTION: DATE: 2001-03-21
FILE REPERENCE: BITRA, 011A
CURRENT APPLICATION NUMBER: G0/206,848
PRIOR APPLICATION NUMBER: G0/206,848
PRIOR APPLICATION NUMBER: G0/206,848
PRIOR APPLICATION NUMBER: G0/206,848
PRIOR APPLICATION NUMBER: G0/206,938
PRIOR PLING DATE: 2000-05-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-10-216
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12706
LENGTH: 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
33.0%; Score 336; DB 9; Length 252;
Best Local Similarity 34.7%; Pred. No. 2.3e-27;
Matches 74; Conservative 47; Mismatches 82; Indels
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; ORGANISM: Staphylococcus aureus
US-09-815-242-12706
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Sequence 1256, Application US/10238075
Publication No. USZ0030148324A1
APPLICATION:
APPLICANTION:
APPLICANTION:
TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat
TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of thei
FILE REPERENCE: BLANDINE
CURRENT APPLICATION NUMBER: US/10/238,075
CURRENT PLING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 0003-16
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 1576
SOFTWARE: Patentin version 3.1
SEQ ID NO 1256
LENGTH: 231
TYPE: PRI

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172 EALRALADK-GATVVVATHSPLFRESADTIIKL 203

RESULT 15 US-10-238-075-1256

1 MIEINDLKKSFGVRILMQGL---SHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQ

62

Gaps

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	Ltd.	
5.1.6	Compugen Ltd.	
GenCore version 5.1.6	- 2004	
GenCore	(c) 1993	
	Copyright	

OM protein - protein search, using sw model

July 27, 2004, 16:33:10 ; Search time 16 Seconds (without alignments) 1220.430 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-868-338-9 1019 1 MIEINDLKKSFGVRILWQGL......VVVATHSPLFRESADTIIKL 203

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			COLUMNIC	
Result No.	Scor	Oυ	ngt.	DB	ID	Description
; ; ; ;	408	: 0		10	1 8	ABC transporter. A
(1)	405	ω.	щ	N	5	hypothetical prote
m	399	39.2	213	7	E95232	ABC transporter, A
4	399	σ.	-	N	30	hypothetical prote
Ŋ	386	۲.	ч	7	20	hypothetical prote
ø	385	۲.	ч	0	78	hypothetical prote
7	380.5	ζ.	Н	0	12	ABC transporter, A
00	80.	7.	4	(1	8	hypothetical prote
σ	~	ů.	N	N	5	ABC transporter (A
10	37	ė.	н	N	99	
11		'n	ø	N	34	glutamine transpor
12	61.	ů.	3	~	9	ABC transporter, A
13	LO	ď.	$\infty$	0	32	ABC transporter AT
14	35	4.	-	7	m	ABC transporter (A
15		4.	N	~	(A)	ABC transporter, A
16	S	4.	2	~	A84109	
17	S	4.	9	7	4	heterocyst maturat
18	3	4.	m	7	$\sim$	c transpo
19	•	4.	0	~	$\sim$	Transporter U
50	49.	4	255	7	$\sim$	ABC-type transport
21	4	4	4	0	021	
22	44	4.	4	Н	482	probable ABC trans
23	34	₩.	m	N	947	ABC transporter, A
24		۳.	щ	~	126	probable ABC trans
25	4	ω,	0	7	142	ABC transporter, A
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27	4	'n.	4	~	560	cal
28	342.5	ω.	~	N	69	porter,
29	42.	ω.	3	Ŋ	3482	porter A

RESULT 2
B97947
hypothetical protein ABC-NBD [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 22-Oct-2001
C;Accession: B97947
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; Es e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, B.J.; Lu, J.; Matsushima, P.; McAhren, S.; McY, P.; Sun, P.M.; Winkler, M.E.

ABC transporter, A	probable ABC trans	hypothetical prote	ABC transporter, A	ABC transporter, A	ABC transporter AT	conserved hypothet	ABC transporter, A	hypothetical prote	ABC transporter (A	ABC transporter, A	hypothetical prote	ABC transporter AT	ABC transporter, A	ABC transporter, A	ABC transporter, A
AC1796	F95337	T47012	AE0237	AI1580	F86843	AF0609	AH1167	D90079	A70074	H72342	H98058	G96929	AG1227	C95192	C97001
N	C)	N	N	~	N	7	7	0	7	7	~	7	~	N	0
207	304	237	237	233	259	648	999	252	257	228	236	238	233	233	234
33.6	33.6	33.5	33.5	33.4	33.3	33.3	33.2	33.1	33.1	33.0	33.0	32.8	32.7	32.7	32.5
342	342	341.5	341.5	340	339	339	338.5	337	337	336	336	334.5	333	333	331
30	31	32	33	34	35	36	37	38	9	40	41	42	43	44	<b>4</b> ,

## ALIGNMENTS

RESULT 1

_	
	Ast transporter, Air-binding protein SPU68/ [imported] - Streptococcus pneumoniae (strair C.Sneries Strantococnus pneumoniae
	C.Date: 03-Aug-2001 #sequence revision 03-Aug-2001 #text change 03-Aug-2001
	C;Accession: G95079
	R; Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
	on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
	nson, T.; Hickey, E.K.; Holt, I.E.
	Determine N. T. Vand R. Cmith H.O. Vanter I.C. Descharts B. N. Morrison
	A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
	A;Reference number: A95000; MUID:21357209; PMID:11463916
	A/Accession: G95079
	A;Status: preliminary
	Aimolecule Type: DNA
	A. (TOSS - FEFFENCES: IZ.1.) < AND AND AND AND AND AND AND AND AND AND
	C; Genetics:
	A;Gene: SP0687
	/ :
	cal Similarity 41.9%; Pred. No. 4.4e-28;
	Matches 88; conservative 44; Mismatches 68; indels 10; Gaps 3;
	CKSFGVRILWQGLSHKFLPGTMTALTGASGSG
	Db 1 MIBLKNISKKFGSRQLFSDWNLHFEGGKLYALIGTSGCGKTTLLNMIGRLBPYDKGQIIY 60
	Qy 61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQ 114
	Db 61 DGTSLKDIFPSVFFRDYLGYLFQDFGLIESQTVKENLALAGLVGKKLKEKEKISLAKQ 117
	Qy 115 VLHAVGLESFE-EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
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	2-
	Db 178 LESLKNPNRTIIATHNPLIWEQVDQVIRV 207
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R.H.; Jaskunas, S.R.;
                                                                                                                                                                                                            B.S.;
                                                                                                        Pypotherical protein ABC-NBD [imported] - Streptococcus pneumoniae (strain R6) (Species: Streptococcus pneumoniae (Species: Streptococcus pneumoniae (Species: Streptococcus pneumoniae (Species: Streptococcus pneumoniae (Species: Streptococcus pneumoniae (Species: Streptococcus pneumoniae (Species: Streptococcus pneumoniae (Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Species: Sp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GB:AE007317; PIDN:AAL00604.1; PID:g15459486; GSPDB:GN00174; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQVLHAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MIBINDLKKSFGVRILMQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV
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; Pred. No. 3.6e-26;
45; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 399; DB 2; L
Pred. No. 2.6e-27;
40; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174 LRALADKGATVVVATHSPLFRESADTIIKL 203
178 LVDLKDENRIIIIATHNPLVWNKADEIIDM 207
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42.9%;
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Best Local Similarity
Matches 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: G98096
A;Status: preliminary
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Residues: 1-213 <. A, Cross-references: C, Genetics: A, Genetics: A, Gene: ABC-NBD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C,Genetics:
A,Gene: SP0111
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Best Local S
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          J. Bacteriol. 183, 5709-5717, 2001
Ajauchors: Yang, Y: Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |: | | : ::|:|||||| || |||:::||:||||| :: 118 ALNRVNLSYLDLKQPIFELSGGBAQRVALAKIILKDPPLILADEPTASLDPRNSEELLSI 177
                                                                                                                                                                        A; Cross-references: GB: AE007317; PIDN: AAK99406.1; PID: 915458184; GSPDB: GN00174
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 DGTSLKDI---KPSVFFRDYLGYLFQDFGLIESQTVKENLNLGLVGKKLKEKEKISLMKQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115 VLHAVGLESFE-EKPVFELSGGEQORTALARVILKNPRIILADEPTGALDLTNSELVIEA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAV-----EKHKWPEIPQ 114
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                                                                                                                                                                                                                                                                                                                                              69; Indels
                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                39.7%; Score 405; DB 2;
41.9%; Pred. No. 7.9e-28;
tive 43; Mismatches 69
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LESLKNPNRTIIIATHNPLIWEQVDQVIRV 207
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A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1987
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Best Local Similarity
Matches 88; Conserv
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Matches 90; Conserv
                                                                                                        A,Accession: B97947
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-213 <KUR>
                                                                                                                                                                                                                                                       A; Gene: ABC-NBD
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A,Cross-references: GB:AE005672; PIDN:AAK76024.1; PID:gl4973462; GSPDB:GN00164; TIGR:SP46
A,Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP1957
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84088
ABC transporter (ATP-binding protein) BH3505 [imported] - Bacillus halodurans (strain C-1)
C;Species: Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Uypotherical protein ABC-NBD [imported] - Streptococcus pneumoniae (strain R6) CiSpecies: Streptococcus pneumoniae CiSpecies: Streptococcus pneumoniae CiSpecies: Streptococcus pneumoniae CiSpecies: Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001 CiAccession: Ost. Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B., R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, Y.; P.; Sun, P.M.; Winkler, M.E.

7, P.; Sun, P.M.; Winkler, M.E.

7, Bacteriol. 183, 5709-5717, 2001
A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, A;Retence number: A97872; MUID:21429245; PMID:11544234
A;Recession: C98093
A;Status: preliminary
A;Molecule type: DMA.
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                                                                                                                                                                                                                                                                                                                                                                                                    1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV
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                                                                                                                                                                                                                                                                                     Length 210;
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                                                                                                                                                                                                                                                                          37.3%; Score 380.5; DB 2; llarity 41.0%; Pred. No. 1e-25; Conservative 41; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 380.5; DB 2;
; Pred. No. 1e-25;
41; Mismatches 72;
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LLSLRDDNRLIIIATHNPAIWEMADEVFIM 206
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                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 86; Conserv
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Matches
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D97884
hypothetical protein ABC-NBD [imported] - Streptococcus pneumoniae (strain R6)
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Species: Streptococcus pneumoniae
C;Accession: D97884
R;Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E
e, R.; Leelland, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, S709-5717, 2001
A;Authors: Yang, Y. Y. Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Authors: Yang, Y. Y. Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Status: preliminary
A;Molecule type: DNA
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AE007317; PIDN:AAK98904.1; PID:g15457636; GSPDB:GN00174
C;Genetics:
A;Genetics:
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G95228
C; Carasporter, ATP-binding protein SP1957 [imported] - Streptococcus pneumoniae (strai C; Species: Streptococcus pneumoniae
C; Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
C; Accession: G95228
S; Tettelin, H; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, Science 293, 498-506, 2001
A; Althors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A; Accession: G95228
A; Accession: G95228
A; Molecule type: DNA
                                                                                                                                                                  61 FGQTNLAVNSAKSQTIIREHISYLFQNFALIDDETVEYNLMLALKYVKLPKKDKLKKVEE 120
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                                                                                                                  EDVDLIKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAV-----EKHKWPBIPQ
                                                                                                                                                                                                                                                  115 VLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEAL
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Best Local Similarity 39.7
Matches 83; Conservative
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ABC transporter, ATP-binding protein homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
C;Accession: D69433
R;Kenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 334-370, 1997
Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Rjitle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor
A;Reference number: A69250; WUID:98049343; PMID:9389475
                                                                                                                                                                                            glutamine transport ATP-binding protein glnQ - Mycoplasma pneumoniae (strain ATCC 29342)
N.Alternate names: hypothetical protein R02_orf465
C;Species: Mycoplasma pneumoniae
A;Variety: ATCC 29342
C;Date: 26-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 02-Feb-2001
C;Accession: S73400
FHImmelacidh, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A;Fitle: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.
A;Reference number: S73327; MUID:97105885; PMID:8948633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Accession: S72400
A, Status: preliminary; nucleic acid sequence not shown; translation not shown
A, Molecule type: DNA
A, Molecule type: LNA
A, Ressidues: 1-465 - HIM>
A, Cross-references: BNBL: AE000009; GB: U00089; NID: 91673720; PIDN: AAB95722.1; PID: 9167372.
A, Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
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C,Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology
C;Keywords: ATP; nucleoxide binding; P-loop
P;23-219/Domain: ATP-binding cassette homology <ABC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C, Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology C, Keywords: ATP, nucleotide binding; P-loop P;251-445, Domain: ATP-binding cassette homology <ABC>P;251-445, Domain: ATP-binding cassette homology <ABC>P;268-275, Region: nucleotide-binding motif A (P-loop)
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181 RQEVDKGKAVVIVTHDSYLKEVSDLVIEI 209
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A; Residues: 1-226 < KLE>
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A;Genetic code: SGC3
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C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 17-May-2002
A;Accession: A84088
R;Takami, H.; Makasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: A84088
A;Accession: A84098
A;Accession: A94098
A;Residues: 1-228 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B86626
BAG transporter ATP-binding protein yabE [imported] - Lactococcus lactis subsp. lactis (5.5pedes: Lactococcus lactis subsp. lactis
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
B;Bolotin, A; Wincker, P; Mauger, S; Jaillon, O; Malarme, K; Weissenbach, J; Ehrli;
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: B86626
A;Actatus preliminary
                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AP001519; GB:BA000004; NID:g10176109; PIDN:BAB07224.1; GSPDB:GN00
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: BH3505
C;Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology
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A;Cross-references: GB:AE005176; PID:g12722846; PIDN:AAK04108.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: yabE
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Matches 82; Conservative
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ABC transporter, ATP-binding protein homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Date: 05-10-1197 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
C;Accession: B69377
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J. Felsichmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-228 *KLE>
A;Cross-references: GB:AE001033; GB:AE000782; NID:g2689356; PIDN:AAB90224.1; PID:g2649576
C;Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology
C;Keywords: ATP; nucleotide-binding motif A (P-loop)
F;23-219/Domain: ATP-binding motif A (P-loop)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 VLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEAL 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 GQILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAV-----EKHKW 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                   34.8%; Score 355; DB 2;
ilarity 37.3%; Pred. No. 1.8e-23;
Conservative 45; Mismatches 80;
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ABC transporter ATP-binding protein / ABC transporter permease protein BMEI0360 [importe C;Species: Brucella meliteneis
C;Species: Brucella meliteneis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AB3297
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AB3685
ABC transporter (ATP-binding protein) BH0281 [imported] - Bacillus halodurans (strain C-C; Species: Bacillus halodurans
C; Species: Bacillus halodurans
C; Date: 0.1-bec-2000 #sequence_revision 01-bec-2000 #text_change 15-Jun-2001
C; Accession: A83685
R; Takami, H; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: GB:AE008917; PIDN:AAL51541.1; PID:g17982259; GSPDB:GN00190 A;Experimental source: strain 16M C;Genetics: C;Genetics: A;Gene: BWB10360 A;Gene: BWB10360 A;Map position: I
                                                                                                                                                                                                                                                                                                                                                                                                                                       |:::: | | | | | | | GEVIINGVKTSGLSDRELTKLRRDSIGFIFQQYNLIPTLTALENVELPMIFRGVARAERE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KWPEIPQVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNS 167
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                                                                                                                                           Length 226;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35.1%; Score 358; DB 2;
39.2%; Pred. No. 2.1e-23;
tive 45; Mismatches 69
                                                                       F;40-47/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 39.2
les 85; Conservative
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Matches 85,
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Mon Aug 2 09:36:56 2004

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Search completed: July 27, 2004, 16:36:52 Job time: 24 secs

us-09-868-338-9.rsp

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GenCore version 5.1.6
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OM protein - protein search, using sw model Run on:

July 27, 2004, 16:29:29 ; Search time 13 Seconds (without alignments) 813.095 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-868-338-9 1019 1 MIEINDLKKSFGVRILMQGL.......VVVATHSPLFRESADTIIKL 203

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

SwissProt\_42:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

P47705 mycoplasma P45022 haemophilus	Q9pdn2 xylella fas	Q8z990 salmonella	P10346 escherichia	Q8zrm9 salmonella	Q8pc11 xanthomonas	Q82wt5 nitrosomona	Q9ck97 pasteurella	P56344 chlorella v	P07109 escherichia
Y467 MYCGE YA78 HAEIN	CYSA_XYLFA	METN_SALTI	GLNQ_ECOLI	METN SALTY	CYSA XANCP	CYSA_NITEU	METN PASMU	CYSA CHLVU	HISP_ECOLI
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27.4	27.2	27.	27.(	27.	26.	26.	26.	26.	26.
279.5 27.4 279 27.4									

## ALIGNMENTS

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                                          POVLHAVGLESFEEKPVFELSGGEQORTALARVILKNPRIILADEPTGALDLINSELVIE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M., Fleischmann R.D., Weidman J.F., Smail K.V., Sandusky M., Fuhrmann J.L., Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M., Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.M., Smith H.O., Hutchison C.A. III, Venter J.C., "The minimal gene complement of Mycoplasma genitalium.";
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PROSITE; PS0693; AEC_TRANSPORTER_2; 1.
Hypothetical protein; ATP-binding; Transport; Complete proteome.
Hypothetical protein; ATP-binding; Transport; Complete proteome.

ATP (POTENTIAL).
CONFILCT 394 399 GDEPTG -> WWWTYW (IN REF. 2).
SEQUENCE 466 AA; 54009 MW; A585044BBA90391C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
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MEDLINE=94075230; PubMed=e253680;
PEPERSON S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
"A survey of the Mycoplasma genitalium genome by using random
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 466;
                                                                                                                                                                                                                                                                                                                                                                                          1973[1], 049281;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Hypothetical ABC transporter ATP-binding protein MG065.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing.";
J. Bacteriol. 175:7918-7930(1993).
-!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.6%; Score 353; DB 1; 39.2%; Pred. No. 2e-22; ative 42; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                    466 AA
                                                                                                                                                                                              411 OFLAIKORYKTIMVIVIHNNLIAQLADLVÍ 440
                                                                                                                                  173 ALRALADK-GATVVVATHSPLFRESADTII 201
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InterPro; IPR003439; ABC transporter.
Pfam, PP00005; ABC tran; 1.
ProDom; PD000006; ABC transporter; 1.
SWART; SM00382; AAA; 1.
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STRAIN-AICC 33530 / G-37;
MEDLINE-96026346; PubMed-7569993;
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EMBL; U02154; AAD12436.1; -.
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les 73; Conserva
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61; Indels 10; Gaps

21 SHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILVEDVDLLKLSTRKQRLYRKNT 80

Conservative

Matches

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261 SHDFI-----VILGPSGSGKTTLLNIISGMDRASSGSVIVNGYNMICLNDRKLTKFRQKY 315
                                                            136
                                                                                                                                                                 Coshima T., Alba H., Baba T. Eujita K., Hayashi K., Honjo A.,

Coshima T., Alba H., Baba T. Eujita K., Hayashi K., Honjo A.,

Ikemcro K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,

Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,

Kamura S., Kitagawa M., Makino K., Mashimoto H., Mishio Y., Saito N.,

Rampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,

An One K., DNA sequence of the Escherichia coli K-12 genome

corresponding to the 12.7-28.0 min region on the linkage map.";

DNA Res. 3:137-155(1996).

IL PUNGTION: Efflux transporter for macrolide antibiotics. Acts in

conjunction with macA.

Conjunction with macA.

IL SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
                                                                                  137 QORTALARVILKNPRIILADEPTGALDITNSELVIBALRALADK-GATVVVATHSPLFRE
                                                            81 VGYLFQDYALIPDRTVKFNLQLAVEKHKWP----EIPQVLHAVGLESFEEKPVFELSGGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIINE-21429237; PubMed-11544226;
Kobayashi N., Nishino K., Yamaguchi A.;
"Novel macrolide-specific ABC-type efflux transporter in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Maybew G.F., Macergor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
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01-NOV-1997 (Rel. 35, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
MACD OR BOR99.
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                                                                                                                                                                                                                              196 SADTII 201
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STRAIN=168 / BGSC1A1;
MEDLINE=55039891; PubMed=7952181;
Yoshida K., Sano H., Miwa Y., Ogasawara N., Fujita Y.;
"Cloning and nucleotide sequencing of a 15 kb region of the Bacillus subtilis genome containing the iol operon.";
Microbiology 140:2289-2298(1994).
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SEQUENCE FROM N.A.
STRAIN=168 / BGS01A1;
MEDIJNE=97021444; PubMed=8867804;
Yoshida K.-I., Fujimyra M., Yanai N., Fujita Y.;
Yoshida K.-I., Fujimyra M., Yanai N., Fujita Y.;
Gloning and sequencing of a 23-kb region of the Bacillus subtilis
genome between the iol and hut operons.";
DNA Res. 2:295-301(1995)
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EMBL; AB071146; BAB64542.1; -

REMBL; AB000189; AAC73966.1; -

REL; D90725; BAA35598.1; -

RIE; D90725; BAA35598.1; -

RIE; COGENE; EG13695; macB.

RICEPPO; IPR003439; AAA ATPase.

INTERPO; IPR003439; ABC transporter.

REAN; PF00005; ABC transporter.

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01-NOV-1995 (Rel. 32, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Hypothetical ABC transporter ATP-binding protein yxdl.
YXDL OR B65F OR BSU39640.
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543 PO'
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417
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648 AA;
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           셤
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248 AA;
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ID Y46B MYCGE
AC Q9ZB70;
                          SEQUENCE
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                                 --LHAV----GLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPIGALDLINSEL 169
                                                                  SIGNATION OF SECULDARY STATES OF THE STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF STATES OF
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J. Bacteriol. 184:5479-5490(2002).
-!- SIMILARITY: Belongs to the ABC transporter family. LolD subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
Fleischmann R.D., Alland D., Elsen J.A., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
"Whole-genome comparison of Mycobacterium tuberculosis clinical and
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PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
Hypothetical protein; ATP-binding; Transport; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Hypothetical ABC transporter ATP-binding protein Rv0986/MT1014.
RV0986 OR MT1014 OR MTV044.14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
Corynebacterinee, Mycobacteriaceae, Mycobacterium.
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Tuberculist; Rv0986; -..
TuterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC_transporter.
Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transporter; 1.
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                                                                                                                                                                  170 VIEALRAL-ADKGATVVVATHSPL 192
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EMBL; AE006985; AAK45262.1; -.
PIR; F70821; F70821
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                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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                                                                                                                                                                4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 QILVEDVDLIKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQL----AVEKHKMPE 111
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STRAIN-ATCC 33530 / G-37;

STRAIN-ATCC 33530 / G-37;

STRAIN-ATCC 33530 / G-37;

STRAIN-ATCC 33530 / G-37;

STRAIN-ATCC 33530 / G-37;

Frain-B-60224346; PubMed=7569993;

Frain-B-602244; PubMed=756, Small K.V., Sandusky M., Fuhramann J.L.,

Pritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhramann J.L.,

Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,

Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;

The minimal gene complement of Mycoplasma gentualium.";
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                                                                                                                                                                                                                                                                          1 MIEINDLKKSFGV----RILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSG
                                                                                                                                                                11; Gaps
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
                                                                                                Length 248;
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical ABC transporter ATP-binding protein MG468.1.
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ATP (POTENTIAL).
711E0BBC872BB81A CRC64;
                                                                                                                                                                80;
                                                                                                DB 1;
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                                                                                        32.3%; Score 329.5; DB 1
35.5%; Pred. No. 9.1e-21;
tive 47; Mismatches 80
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Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transporter; 1.
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Interpro; IPR003439; ABC_transporter.
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27373 MW;
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                                                                                                                                                                       Conservative
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us-09-868-338-9.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kunst F., Gasawara N., Mosser I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Azevedo V., Bertero M.G., Brans A., Braun M., Brignell S.C., Bron S., Broullet S., Bruschi C.V., Cadawell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Anian K.D., Errington J., Pabret C., Frarizi B., Foulger D., Brian K.D., Errington J., Pabret C., Frarizi B., Foulger D., Anis B., Kulita M., Pujita M., Golightly E.J., Grandi G., Guiseppi G., Guy B.J., Haga K., Haicch J., Harwod C.R., Henaut A., Hilbert H., Holsappel S., Rosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C., Achayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Porterelle D., Porwollik S., Perscott A.M., Porteclel D., Porwollik S., Perscott A.M., Persecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
                                                                                                                                                                                                                                                                                                                                                                                                         14 RILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILVEDVDLLKLSTRKQ 73
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STRAIN=168 / JH642;
STRAIN=168 / JH642;
MEDLINE=97124195; PubMed=8969508;
Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M., Kobayashi Y.;
Kobayashi Y.;
"Systematic sequencing of the 283 kb 210 degrees-232 degrees region of the Bacillus subtilis genome containing the skin element and many spornLation genes.";
Microbiology 142:3103-3111(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 RLYRKNTVGYLFODYALIPDRTVKFNLQLA -- VEKHKWPEIPQVLHAVGLESFEEKPVFE
                                                                                                                                                                                                                                                                                                                                    Gaps
SWART; SM00382; AAA; 1.
PROSITE; PS0021; ABC_TRANSPORTER_1; 1.
PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
Hypothetical protein; ATP-binding; Transport; Complete proteome.
NP_BIND
NP_BIND
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ATP (POTENTIAL).
ATP-ATP (POTENTIAL).
ATP-ATP (POTENTIAL).
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01-0CT-1996 (Rel. 34, Last sequence update)
10-0CT-2003 (Rel. 42, Last amoration update)
Probable amino-acid ABC transporter ATP-binding protein yqiz.
                                                                                                                                                                                                                                                            Query Match
31.9%; Score 325.5; DB 1; Length
Best Local Similarity 36.3%; Pred. No. 2.3e-20;
Matches 70; Conservative 44; Mismatches 76; Indels
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
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MEDLINE=98044033; PubMed=9384377;
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EKIVELAKRVIKI 261
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Interpro; IPR003593; AAA\_Arpase.
Interpro; IPR003593; AAG\_transporter.
ProDom; PR00006; ABC tran; 1.
ProDom; PR00006; ABC transporter; 1.
SNART; SN00382; AAA; 1.
PROSITE; PS0081; AAC\_TRANSPORTER 1; 1.
PROSITE; PS0083; ABC\_TRANSPORTER 2; 1.
HYPOTHAETICAL procein; ATP-binding; Transport; Membrane; Complete proteome.
NP\_BIND 72; Indels Y352 THEMA STANDARD; PRT; 234 AA.
Q9WYI7;
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2004 (Rel. 43, Last annotation update)
TMO352.
Thermotoga maritima. NP BIND 34 41 ATP (POTENTIAL). SEQUENCE 240 AA; 26949 MW; B559DA39D6C3BAAB CRC64; 61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNL----167 SELVIEALRALADKGATVVVATHSPLF-RESADTII 201 172 VKEVLQVMKELVETGMTMVIVTHEMGFAKEVADRVL 207 / Match 31.9%; Score 325; DB 1; Local Similarity 36.6%; Pred. No. 2.1e-20; nes 79; Conservative 41; Mismatches 72; Query Match X352 THEMA Y352 THEMA ID Y352 TO DT 16-OCT DT 15-OCT DT 15-OCT DT 15-OCT DT HYPOTH GN TM0352 OS Thermo SOLUTION TO THE PROPERTY OF TH ò 셤 ઠ 셤 8

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DB 1;
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01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
ABC transporter ATP-binding protein MJ0796.
MG1796.
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STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
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Q58206;
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SEQUENCE
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AC Q58206
DT 01-NOV
DT 10-OCT
DD ABC tr
GN MJ0796
OS Methan
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                                                                                                              STRAIN=MSBB / DSM 3109 / ATCC 43589,
MEDLINE=9287316; PubMed=10366571;
Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Faledalberg S.L., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 QGLSHKFLPGTMTALTGASGSGKSTLINCLGTLDKPSSGQILVEDVDLLKLSTRKQRLYR
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Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
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InterPro; IPR003439; ABC_transporter.
Pfam; PPR00005; ABC_tran; 1.
Probom; PR000006; ABA; 1.
PROSTIE; PS00211; ABC_TRANSPORTER 1; 1.
PROSTIE; PS00211; ABC_TRANSPORTER 2; 1.
Hypothetical protein; ATP-binding; Transport; Complete proteome.
NP_BIND
41 48 ATP-binding; Pransport; Complete proteome.
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical ABC transporter ATP-binding protein MG468.1 homolog
(KOS orf284).
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Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
NCBI_TaxID=2104;
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                                                                                                                                                                                                                                                                                                                                                                                                            genome sequence of Thermotoga maritima.";
Nature 399:323-329(1999).
-!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8A762A4852BF08D5 CRC64;
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Matches 71; Conservative
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                                 NCBI_TaxID=2336;
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Q50316;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 --RNKNVGYIFQQYGLLRDLNVDDNIKLAVPFKKRHNNNLEELLERLELKEHRNKKITKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete sequence analysis of the genome of the bacterium Mycoplasma
[1]
SECURICE FROM N.A.
STRAIN=ATCC 29342 / M129;
STRAIN=ATCC 29342 / M129;
MEDLINE=96177562; PubMed=8604303;
Hilbert H., Himmelreich R., Plagens H., Herrmann R.;
"Sequence analysis of 56 kb from the genome of the bacterium Mycoplasma pneumoniae comprising the dnaA region, the atp operon and a cluster of ribosomal protein genes.";
Nucleic Acids Res. 24:628-639(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR, $62839; $62839.
InterPro; IPR003439; AAA_ATPase.
InterPro; IPR003439; ABC_transporter.
Pfam, PP00005; ABC_tran; I.
ProDom; PD000006; ABC_transporter; I.
PROSITE; PS00211; AAA; I.
PROSITE; PS00211; ABC_TRANSPORTER 1; I.
PROSITE; PS50893; ABC_TRANSPORTER 2; I.
Hypothetical protein; ATP-binding; Transport; Complete proteome.

APP (POTENTIAL).

APP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996).
-!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 AA; 32241 MW; E2275C81CFE295E0 CRC64;
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KHKWPEIPQVLHAVGLESFEE----KPVFELSGGEQQRTALARVLLKNPRIILADEPTG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=562;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8680807;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Tomb J.-F., Adams M.D., Reiche J.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Kougherty B.A., Tomb J.-F., Adams M.D., Reiche C.I.,

Overbeek'R., Kirknes M.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The crystal structure of the MJ0796 ATP-binding cassette. Implications for the structural consequences of ATP hydrolysis in the active site of an ABC transporter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yuan Y.-R., Blecker S., Martsinkevich O., Millen L., Thomas P.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-ZAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF MUTANT GLN-171.
MEDLINE=22146558; PubMed=12150914;
Smith P.C., Karpowich N., Millen L., Moody J.E., Rosen J.,
Thomas P.C., Hunt J.F.,
"ATP binding to the motor domain from an ABC transporter drives formation of a nucleotide sandwich dimer.";
Mol. Cell 10:139-149(2002).
-! SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transporter.
Pfam; PP000005; ABC_tran; 1.
Probon; PD000006; ABC_transporter; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER 1; 1.
PROSITE; PS50893; ABC_TRANSPORTER 2; 1.
Transport; ATP-binding; Complete protecome; 3D-structure.
NP_BIND
38
45
ATP (POTENTIAL).
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   Archaea, Buryarchaeota, Methanococci, Methanococcales, Methanocaldococcaceae, Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
MEDLINE=21402895; PubMed=11402022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 276:32313-32321(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U67524; AAB98791.1; -.
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Best Local Similarity 34.0.
Best Local 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; D64399; D64399.
PDB; 1F30; 25-JUL-01.
PDB; 1L2T; 24-JUL-02.
TIGR; MJ0796; -
                                                                          NCBI_TaxID=2190;
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121 RRK----RALECLKMAELEERFANHKP-NQLSGGQQQRVAIARALANNPPILLADEPTG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-11, AND CHARACTERIZATION.
MEDLINE=20245870; PubMed=10783239;
Yakushi T., Masuda K., Narita S., Matsuyama S., Tokuda H.;
Yakushi T., Masuda K., Narita S., Matsuyama S., Tokuda H.;
Yakushi T., Masuda K., Narita S., Matsuyama S., Tokuda H.;
Yakushi T., Masuda K., Narita S., Matsuyama S., Tokuda H.;
Ipiproteins from membranes...
In w. ABC transporter mediating the detachment of lipid-modified proteins from membranes. Such an Arp-dependent transport system responsible for the release of lipporceins targeted to the outer membrane for the inner membrane. Such a release is dependent of the sorting-signal (absence of an Asp at position 2 of the mature lipporcein) and of lola.
-!- SIBCELLULAR LOCATION: Inner membrane-associated.
-!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-RIZ / MGGE55;
MEDLINE=97426617; Pubmed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                  161 ALDLINSELVIEALRALADK-GATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                       LOLD ECOLI STANDARD; PRT; 233 AA.
P75.97; OBRNN6;
P75.97; OBRN6;
15.00V-1998 (Rel. 35, Created)
15.0EC-1998 (Rel. 37, Last sequence update)
15.0EC-1998 (Rel. 43, Last annotation update)
Liboprotein releasing system ATP-binding protein lolD.
                                                                                              EMBL; AE000212; AAC74201.1; ALT INIT. EMBL; D90747; BAA35937.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=K12;
MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EcoGene; EG13440; lolD.
Interpro; IPR003593; AAA_ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Res. 3:137-155(1996).
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                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli.
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7;

Indels

Length 233;

DB 1;

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                                                                                                                                                                                                                                                                                                                                                                                               87 DYALIPDRIVKFN--LQLAVEKHKWPEIP----QVLHAVGLESFEEKPVFELSGGEQQRT 140
                                                                                                                                                                                                                                                                                                                                                                                                                          27 GTWTALTGASGSGKSTLLNCLGTLDKPSSGQILVEDVDLLKLSTRKQRLYRKNTVGYLFQ 86
                                                                                                                                                                                                                                                                                                                                    GEMMAIVGSSGSGKSTLLHLLGGLDTPTSGDVIFNGQPMSKLSSAAKAELRNQKLGFIYQ 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAINSJALS - | DSM 2661 / ATCC 43067;
MIDEJON - | DSM 2661 / ATCC 43067;
MIDEJON - | DUBM648680807;
BULL C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Scutton G.G., Rirkness B.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Puhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klank H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 ALARVLLKNPRIILADEPTGALDLTNSELVIBALRALAD-KGATVVVATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical ABC transporter ATP-binding protein MJ1508.
                                                                                                                                                                            SEQUENCE 233 AA; 25438 MW; 1C305476182F1EFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the ABC transporter family.
InterPro, IPR003439, ABC_transporter.
Pfam; PF00005, ABC_tran; 1.
ProDom; PD000006; ABC_transporter; 1.
SMAR; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS00833; ABC_TRANSPORTER_2; 1.
ATP-inding; Transport; Complete protecome.
NP_BIND
ATP (BY SIMILARITY)
                                                                                                                                                                                                                         30.4%; Score 309.5; DB 1
42.4%; Pred. No. 4.1e-19;
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                                                                                                                                                                                                                                                                31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC transporter.
Pfam. PF000005; ABC tran; 1.
SProDom; PD0000006; ABC transporter; 1.
SWART; SM00382; AAA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U67591; AAB99520.1; -. PIR; C64488; C64488.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          jannaschii.";
Science 273:1058-1073(1996).
                                                                                                                                                                                                   Methanococcus jannaschii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=2190;
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(7
                                                                                                                                                                                                                                                                               57 QILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAV-----EKHKWP 110
                                                                                                                                                                                                                                                                                                                                                       111 EIPQVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELV 170
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Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Heidelberg J.F., Eisen J.A., Nelson W.C., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salbberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                         :: : : | :: | :: | :: | :: | EVYYKGRRISSMSENERAIFRRKISGFIFQOFHLIKTLIALENVELPMMLDERDKSYRRK
                                                                                                                                                                                                     1 MIBINDLKKSFG----VRILWQGLSHKFLPGTWTALTGASGSGKSTLLNCLGTLDKPSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 406:477-483(2000).

-!- FUNCTION: Part of the binding-protein-dependent transport system macNIQ for D-mathionine. Probably responsible for energy coupling to the transport system (By similarity).
-!- SUBCELLULAR LOCATION: Inner membrane-associated (Potential).
-!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                Gaps
PROSITE; PS00211; ABC TRANSPORTER 1; 1.
PROSITE; PS50893; ABC TRANSPORTER 2; 1.
Hypochetical protein; Transport; ATP-binding; Complete proteome.
NP BIND 38
SEGUENCE 224 AA; 25263 MW; CF0B72742D24921E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                10;
                                                                                                                         Length 224;
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Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                              90; Indels
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Probable D-methionine transport ATP-binding protein metN.
                                                                                                                     ch 30.3%; Score 309; DB 1; 1 Similarity 34.3%; Pred. No. 4.4e-19; 73; Conservative 40; Mismatches 90.
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Interpro, IPR003439, ABC_transporter.
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STRAIN=El Tor N16961 / Serotype Ol;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 KHKWPEIPQVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADBPTGALDLT 165
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                                                                                                                                                                                                                                                                                                 1 MIEINDLKKSFGVRILWQGLS-----HKFLP-GTMTALTGASGSGKSTLLNCLGTLD
                                                                                                                                                                                                                                                                                                                                       1 MIBIKSVNKVF-----YQGDKQIHALKDINLFIPQGTIFGVIGSSGAGKSTLIRCVNMLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97124189; PubMed=8969502;
Yamane K., Kumano M., Kurita K.;
Yamane K., Kumano M., Kurita K.;
The 25 degrees-16 degrees region of the Bacillus subtilis
chromosome: determination of the sequence of a 146 kb segment and
identification of 113 genes.";
Microbiology 142:3047-3056(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=56004473; PubMed=7551042;
Rodriguez F., Grandi G.;
"An operon encoding a novel ABC-type transport system in Bacillus
                                                                                                                                                                                                                                                         22;
Pfam; PF00005; ABC tran; 1.

Prodom; PD000006; ABC transporter; 1.

SMART; SM0382; AAA; 1.

PROSITE; PS00211; ABC TRANSPORTER_1; 1.

PROSITE; PS50833; ABC TRANSPORTER_2; 1.

Transport; Amino-acid transport; ĀTP-binding; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
10-CCT-2003 (Rel. 42, Last annotation update)
Probable amino-acid ABC transporter ATP-binding protein yckI.
                                                                                                                                                                                                                 Length 344;
                                                                                                                                                                                                                                                       65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                    40D60D2C0CF52913 CRC64;
                                                                                                                                                                                                            30.3%; Score 309; DB 1;
36.1%; Pred. No. 7.2e-19;
iive 44; Mismatches 65
                                                                                                                                                  (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 TTQSILELLKEINROLNLTILLITH 199
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                                                                                                                                                  ATP
                                                                                                                                                NP BIND 38 45 A SEQUENCE 344 AA; 37574 MW;
                                                                                                                                                                                                                                Local Similarity 36.19
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                                                                                                                                 Complete proteome.
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RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., RA Bourise L., Brans A., Braun M., Brignell S.C. Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choil S.K., Codani J.G., Connerton I.F., Cummings N.J., Daniell R.A., RA Entian K.D., Brington J., Fabret C., Ferrari E., Foulger D., Frington J., Fabret C., Ferrari E., Foulger D., RA Entian K.D., Erington J., Fabret C., Ferrari E., Foulger D., RA Entian K.D., Erington J., Fabret C., Ferrari E., Foulger D., RA Entian S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G., Guy B.J., Baga K., Haiech J., Harwood C.R., Henaut A., RA Hibbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., RA Kobayashi Y., Koetter P., Kohlingstein G., Krogh S., Kumano M., Koetter P., Kohlingstein G., Krogh S., Kumano M., Kolein C., RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., RA Medina N., Mellado R.P., Mizuno M., Mosell D., Nakai S., Noback M., RA Presecan B., Poll T.M., Porterelle D., Porwollik S., Perscott A.M., RA Presecan B., Pulic P., Purnelle B., Rapoport G., Rey M., Reynolds S., Schoetter R., Soffene F., Schoette R., Schoette R., Schoette R., Schoette R., Schoette R., Schoette R., Schoette R., Schoette R., Schoette R., Schoette R., Schoette R., Schoette R., Schoette R., Stone B., Voshida S., Yandehol M., Vannier P., Vassarotti A., Tanaka T., Tarkahashi H., Takemaru K., Takaka H., Yamane K., Yasarotti A., Yandenco M., Wobhida K., Yandeler E., Wedler H., Weitzenegger T., RA Winters P., Winget A., Yandelen B., Yoshikawa H., Danchin A., Tarkana, R., Yandeler E., Wedler H., Weitzenegger T., R., Webrilse, M., Wenneller B., Yoshikawa H., Danchin A., Tarkana, M., Yander B., Yoshikawa H., Danchin A., Tarkana, M., Yander B., Yoshikawa H., Danchin A., Tarkana, M., Yander B., Yoshikawa S., Weber B., Yoshikawa S., Weber B., Yoshikawa S., Weber B., Yoshikawa S., Weber B., Yoshikawa S., Weber B., Yoshikawa S., Weber B., Yoshikawa S., Weber B., Yoshikawa S., Yoshikawa S., Yoshikawa S., Yoshikawa S., Yoshikawa S., Yoshik
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MEDLINE=93360913; PubMed=8355609;
MEDLINE=93360913; PubMed=8355609;
MEDLINE=93360913; PubMed=8355609;
MEDLINE=93360913; PubMed=8355609;
Wenema G., van Sinderen D.;
"Sequence and analysis of the genetic locus responsible for surfactin synthesis in Bacillus subtilis.";
MOI. Microbiol. 8:811-831(1993).
-!- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
-!- FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT
-!- SYSTEM FOR AN AMINO ACID. PROBABLY RESPONSIBLE FOR ENERGY COUPLING
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SQVSPV (1N REF. 2).
P -> G (1N REF. 1 D08F42F2B3490A7D CRC64;
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PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
ATP-binding; Transport; Complete proteome.
ATP-binding; 34
41
ATP (POTENTIAL).
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EMBL, D50453; BAA08992.1; -
EMBL, 299105; CAB12153.1; -
EMBL, X70356; -; NOT ANNOTATED_CDS.
PIR, C69761; C69761.—ANNOTATED_CDS.
Subtilists; BG1185; YGKI.
InterPro; IPR003593; AAA ATPASE.
R InterPro; IPR003439; ABC_transporter.
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ProDom; PD000006; ABC transporter; 1.
SMART; SM00382; AAA; 1.
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RAM KUNST F., Ogsaawara N., Moszer I., Albertini A.M., Alloni G.,

Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Brouilet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Brouilet S., Bruschi C.V., Coldwell B., Capuano V., Carter N.M.,

RA Brouilet S., Brington J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Broisof S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

RA Choi S.K., Devine K.M., Dusterhoff A., Ehrlich S.D., Emmerson P.T.,

RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,

RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,

Antibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,

A Coris B., Karamata D., Kasahara Y., Klarr-Blanchard M., Klein C.,

A Cobyashi Y., Koctter P., Koningstein G., Radgue C.,

A Kobayashi Y., Koctter P., Koningstein G., Madigue C.,

A Kobayashi Y., Mizuno M., Mosetl D., Nakai S., Noback M.,

Noone D., O'Reilly M., Ogawa K., Odiwara A., Oudega B., Park S.H.,

Rator V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,

Parro V., Pohl T.M., Portetelle D., Porwollik S., Ray M., Raynolds S.,

Resecan B., Pujie P., Purnelle B., Roce M., Sadaie Y.,

Reseron B., Tacconi E., Takagi T., Takabashi H., Takemaru K.,

Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,

Tosato V., Wambutt R., Wedler E., Wadler H., Waitzenegger T.,

Winters P., Wipat A., Yamamoto H., Yamier K., Yasatotti A.,

Winters P., Wipat A., Yamamoto H., Yamier K., Yasatotti A.,

Wandut R., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;

Poshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
                                                                                                                                                                                                              107 HKWPEIP----QVLHAVGLESFEEXPVFELSGGEQORTALARVLLKNPRIILADEPTGAL 162
                                                                                                                                                                                                                                    61 ED------VDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQ---LAVEK 106
                                                                                                                                                                           61 DDFSIDFSKKVKQADILKIR-----RKSPM--VFQAYHLFPHRTALENVMEGPVQVQK 111
                                                                      1 MIBINDLKKSFGVRILMOGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60
                                                                                                      9
                                                                                             34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=168 / BGSC1A1;
STRAIN=168 / DidNed=8867804;
STRAIN=168 / DidNed=8867804;
STRAIN=10.7 Fujimya W., Yanai N., Fujita Y.;
"Cloning and sequencing of a 23-kb region of the Bacillus subtilis genome between the iol and hut operons.";
[2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Probable amino-acid ABC transporter ATP-binding protein yxeO.
YXEO OR LP9G OR BSU39480.
Bacillus subtilis.
Length 247;
ch 29.7%; Score 303; DB 1; Length 24 I Similarity 37.7%; Pred. No. 1.6e-18; 84; Conservative 35; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                   DLTNSELVIEALRA---LADKGATVVVATHSPLF-RESADTII 201
                                                                                                                                                                                                                                                                                                     D---PELVGEVLKVIKDLANEGWIMVVVTHEIKFAQEVADBVI 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                            249 AA
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                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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   Query Match
Best Local 9
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YXEO BACSU
                                     Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 KRIGMEILKQVGLEHKADSYPITMSGGQQQRIGIARALAVNPHAILLDEPTSALDPELVT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MIEINDLKKSFGVRILWQGLSHKFLPGTWTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 ----QVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 EDVDL-LKLSTRKORLYRKNTVGYLFQDYALIPDRTVKFNL--QLAVEKHKWPEIP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GEAKLNAEKFTRKEAHRLRQQTAMVFQNYNLFKNKTALQNITEALIVAQHK----PRDEA
complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                       FUNCTION: PROBABLY PART OF A BINDING-PROTEIN-DEPENDENT TRANSPORT SYSTEM FOR AN AMINO ACID. PROBABLY RESPONSIBLE FOR ENERGY COUPLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 249;
                                                                                                                                                  TO THE TRANSPORT SYSTEM.
-!- SUBCELLULAR LOCATION: Membrane-associated (Potential).
-!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PSO0211; ABC_TRANSPORTER_1; 1.
PROSITE; PSS0893; ABC_TRANSPORTER_2; 1.
Hypothetical protein; ATP-binding; Transport; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 41 ATP (POTENTIAL).
249 AA; 27742 MW; A63886EDE69AB80B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.7%; Score 302.5; DB 1
34.6%; Pred. No. 1.7e-18;
iive 42; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169 LVIEALRALADKGATVVVATHSPLF-RESADTII 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, D45912; BAA08331.1; -.
EMBL, Z99124; CAB15984.1; -.
PIR, A70076; A70076.
Subtlist; B611891; yxe0.
InterPro; IPR003593; AAA ATPase.
InterPro; IPR003439; ABC transporter.
Pfam, PF000005; ABC transporter.
ProDom; PD000006; ABC transporter.
SMART; SM00382; AAA; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 34.v..
A4, Conservative
                                                          Nature 390:249-256(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete proteome.
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			17 36
	GenCore version		18
	Copyright (c) 1993 - 2004 Compugen Ltd.		0.0
			21 35
OM protein - pr	OM protein - protein search, using sw model		22. 35
Run on:	July 27, 2004, 16:32:35; Search time 38 Seconds		
	(Without alignments) 1685.531 Million cell updates/sec		25 35
Title:	US-09-868-338-9		28 35
Ferrect score:	1012 1012 1013 1013 1013 1013 1013 1013		א כ
educa:	vvvainsturksadiinu		31
Scoring table:	BLOSUM62		32 35
	Gapop 10.0 , Gapext 0.5		
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Searcheu:	TOTIOTI BEGS, SIDDIOZOZ FEBIGUES		
Total number of	Total number of hits satisfying chosen parameters:		37
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Minimum DB seg	seq length: 0		39
Maximum DB seq	length: 2000000000		
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Post-processing	Post-processing: Minimum Match 0%		
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Database :	SPTREMBL 25:*		
	1: sp archea:*		
	2: sp_bacteria:*		
	3: sp_fungi:*		
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		RESULT	LT 1
	6: sp_mammal:*	Q93ME0	IE0
	7: sp_mhc:*	95	O93MEC
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	v: sp phage: *	T C	01-DEC
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		8	Plasmi
	16: sp_bacteriap:*	0	Bacter
	17: sp_archeap:*	)	Clost

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Q93me0 clostridium O97ru9 streptococc	Q892j8 clostridium	Q9zhbl streptococc	Q8dgm3 streptococc	Q97nn3 streptococc	Q8dnd2 streptococc	Q97t44 streptococc	Q8dri7 streptococc	Q91650 lactococcus	Q97nrl streptococc	Q8dnf2 streptococc	Q9k767 bacillus ha	Q9cji3 lactococcus	Q93h50 streptomyce	.09ac69 staphylococ
SUMMARIES	Q93ME0	089248	Q9ZHB1	ОВБОМЗ	Q97NN3	QBDND2	Q97T44	Q8DRI7	Q9L650	Q97NR1	QBDNF2	Q9K767	Q9CJ13	Q93H50	Q9AC69
DB	16	16	0	16	16	16	16	16	N	9₹	16	16	16	16	16
% Query Match Length DB	211	212	213	213	213	213	213	213	207	210	210	228	211	248	208
% Query Match	40.3	9.00	39.8	39.7	39.2	39.2	37.9	37.8	37.5	37.3	37.3	36.8	36.6	36.5	35.9
Score	411	407	406	405	399	399	386	385	382	380.5	380.5	375	373	371.5	366
Result No.	110	ım	4	2	9	7	80	0	10	TT	12	13	14	15	16

archaeoglob				fusobacteri	streptomyce	streptococc	bacillus ha			streptococc									υ	streptococc	Ø	streptococc	archaeoglob	campylobact	clostridium	lactobacill	pasteurella	listeria mo
028803	Q831r7	Q973j6	Q8yit2	Q8rdy9	6,016Q	Q8p0u2	Q9kg34	029244	Q9k6q5	Q99zf0	Q81hp0	Q97iv5	Q8k7b3	Q878p3	Q9pr26	Q971x2	72xn60	Qaptba	Q8xme3	Q8e5m1	Q8dzx1	Q99xu3	028456	O9pm14	Q894w5	Q88uis	Q9cni3	Q8y3q9
028803	083LR7	0973J6	Q8YIT2	Q8RDY9	Q9L0J9	QBPOUZ	Q9KG34	029244	Q9K6Q5	Q992F0	Q81HP0	Q971V5	Q8K7B3	Q878P3	Q9PR26	Q971X2	Q9UX77	Q8PTP8	Q8XME3	Q8E5M1	Q8DZX1	Q99XU3	028456	Q9PM14	Q894W5	Q88UI5	Q9CNI3	Q8Y3Q9
17	16	17	16	16	16		16	17	16	16	16	16	16	16	16	16	17	17	16	16	16	16	17	16	16	16	16	16
226	648	232	381	224	246	233	213	228	227	233	216	232	233	237	300	255	246	265	233	250	250	224	231	217	227	664	227	207
7. 7.		35.3		'n.	'n.	4.	4,						34.4	34.4	34.4	34.3	4.	34.2						33.9	۳,		m	33.8
361.5	m	360	358	57	356.5	356	355	354.5	353	352	351.5	351	351	351	50	349.5	349	348.5	348	348	348	346	346	4	45.		44.	344
17	18	19	20	21	22.	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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Length 211;

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115 VLHAVGLESFE-EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 VLKOMNLEGYEKRKIFELSGGEQORVSIARLLIKPSKIIIADEFIGSLDAKNRDLVLYYL 182
61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAV-----EKHKWPEIPQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 EDVDLIKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAV-----BKHKWPEIPQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ABC) transporter acti. . .; IEA
                                     1 MIEINDLKKSFGVRILMQGLSHKFLPGTWTALTGASGSGKSTLLNCLGTLDKPSSGQILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 IVKMENITKKFGDKIILNNFSLDIQDGELLAVTGASGSGKSTILNIGLLEGFDSGKLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 VLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The genome sequence of Clostridium tetani, the causative agent tetanus disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Massachusetts / E88;
MEDLINE-22457253; PubMed=12552129;
Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang F
Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
Gottschalk G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complete protecme. SS903 MW; B57A58ECBD6152E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cecanda disease.; V.S.A. 100:1316-1321(2003).

EMBL; AE015943; AA036597.1; -...

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005524; F:ATP binding; IEA.

GO; GO:0004009; F:ATP-binding cassette (ABC) trans

GO; GO:0006810; P:transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.9%; Score 407; DB 16; 42.6%; Pred. No. 1.8e-25;
                                                                                                                                                                                                                                                        212 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46; Mismatches
                                                                                                                                                                                                                          174 LRALADKGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PEGM; PF00005; ABC tran; 1.
PROSITE; PS00211; ABC TRANSPORTER 1; 1.
PROSITE; PS50893; ABC TRANSPORTER 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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01-JUN-2003 (TrEMBLrel. 24,
01-JUN-2003 (TrEMBLrel. 24,
01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clostridium tetani.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transporter.
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                                             1;
                                                                                                                                                                                                115 VLHAVGLESFEEKPVFELSGGEQORTALARVLLKNPRIILADBPTGALDLTNSELVIEAL 174
                                                                                                                                                                         61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVE-----KHKWPEIPQ 114
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GO; GO:0016020; F: ATP binding; IEA.
GO; GO:0005524; F: ATP binding; Cassette (ABC) transporter acti. . .; IEA.
GO; GO:000166; F: Tauclectide binding; IEA.
GO; GO:000166; F: Tauclectide binding; IEA.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003593; AAA_ATPase.
FinterPro; IPR003593; ABC transporter.
Fam; ProDom; PD000006; ABC transporter.
FroDom; PD000006; ABC transporter.
SWART; SW00382; AAA; InterPropress 1.1
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                                             Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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Last annotation update)
  40.3%; Score 411; DB 16;
40.2%; Pred. No. 8.2e-26;
iive 52; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                               175 RALADKGATVVVATHSPLFRESADTIIKL 203
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PROSITE; PS5083; ABC TRANSPORTER 2; 1.
PROSITE; PS5083; ABC TRANSPORTER 2; 1.
SEQUENCE 213 AA; 24002 MW; DBAD86F4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-07T-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequ
01-0CT-2003 (TrEMBLrel. 25, Last anno
ABC transporter, ATP-binding protein.
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Science 293:498-506(2001).
EMBL; AE007378; AAK74832.1;
PIR; G95079; G95079.
TIGR; SP0687; --
Query Match
Best Local Similarity 40.2<sup>3</sup>
Matches 84; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                            183
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Query Match 39.7%; Score 405; DB 16; Length 2: Best Local Similarity 41.9%; Pred. No. 2.6e-25; Matches 88; Conservative 43; Mismatches 69; Indels
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Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
Streptococcus.
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01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter, ATP-binding protein.
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01-MAR.2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter ATP-binding protein-sodium transport.
ABC-NBD OR SPR0602.
Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobaciliales; Streptococcaceae;
Streptococcus.
NCBI_TAXID=171101;
                                                                                                               O'THAY-1999 (TrEWBLrel. 10, Created)
01-MAY-1999 (TrEWBLrel. 10, Last sequence update)
01-OCT-2003 (TrEWBLrel. 25, Last annotation update)
Hypothetical protein:
Streptococcus preumoniae.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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SEQUENCE FROM N.A.
MEDLINE=21429245; PubMed=11544234;
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                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus
ОВБОМЗ
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61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAV-----EKHKWPEIPQ 114 61 DGTSLKDI----KPSVFFRDYLGYLFQDFGLIBSQIVKENLNLGLVGKKLKEKEKISLMKQ 117 115 VLHAVGLESFE-EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173 RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., Beloff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C., Radimour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E.,

A Limbur R., Glass J.S., Khoja H., R.Z., Lu J., Matsushima P.,

B. Leblanc D.J., Lee L.N., Leffwaitz E.J., Lu J., Matsushima P.,

RA Morhis F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,

RA Jook C.A., Baltz R.H., Jaskunas S.R., Young-Bellido M., Zhao G.,

Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,

RA Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,

RA Joseph J. J.,

R J. Bacteriol. 183:5709-5717(201).

R PIR, B97947; B97947.

CO; GO:000520; C:membrane; IRA.

CO; GO:000520; C:membrane; IRA.

CO; GO:000520; C:membrane; IRA.

CO; GO:000520; P:ATP-binding; Cassette (ABC) transporter acti. . .; IEA.

CO; GO:000520; P:ATP-binding; IEA.

CO; GO:000520; P:ATP-binding; IEA.

CO; GO:000620; P:ATP-binding; IEA.

CO; GO:000620; P:ATP-binding; IEA.

CO; GO:000620; ABC\_transporter.

CO; GO:000620; ABC\_transporter.

CO; GO:000620; ABC\_transporter.

CO; GO:000620; ABC\_transporter.

CO; GO:000620; ABC\_transporter; 1.

CO; GO:000620; ABA; I.

RPOSITE; PS00021; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABC\_transporter; 1.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABC\_transporter; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABC\_transporter; I.

CO; GO:000620; ABC\_transporter; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:000620; ABA; I.

CO; GO:0006 1 MIELKNISKKFGSRQLFSDTNLHPEGGKIYALIGTSGCGKTTLLNMIGRLEPYDKGQIIY 60 SEQUENCE FROM N.A.

STRAIR=ATCC BAA-334 / TIGR4;

MEDLINB=21357209; Pubbed=11463916;

Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,

Tettelin H., Nelson K.E., Paulsen I.T., Haft D.H., Dodson R.J.,

Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,

Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,

Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,

McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,

Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C., 1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV

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MEDLINE-21357209; PubMed=11463916;

Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,

Peterson S., Heidelberg J., Daulsen I.T., Haft D.H., Dodson R.J.,

Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,

Umayam L.A., Wilte O., Salzberg S.L., Lewis M.R., Radune D.,

Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,

McDonald L.A., Feldblyum T.V., Angluoli S., Dickinson T., Hickey I

Holt I.E., Loftus B.J., Marrison D.A., Mollingshead S.K., Fraser C.M.;

Complete genome sequence of a virulent isolate of Streptococcus
GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti.
GO; GO:000616; F:nuclectide binding; IEA.
GO; GO:000610; P:transport; IEA.
InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transporter.
Probom; PR00006; ABC_transporter.
Probom; PR00006; ABC_transporter; 1.
SMART; SM00312, AAA, I.
PROSITE; PS00211; ABC_TRANSPORTER 1; 1.
PROSITE; PS00893; ABC_TRANSPORTER 2; 1.
ATP-binding; Complete protecome.
SEQUENCE 213 AA; 23920 MW; FGBEZEA4EE87FDB7 CRC64;
                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                               39.2%; Score 399; DB 16; Length 213; 42.9%; Pred. No. 7.9e-25; vative 40; Mismatches 70; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
ATP-binding protein, putative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 LVDLKDENRIIIATHNPLVWNKADEIIDM 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 AA.
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01-0CT-2001 (TrEMBLrel. 18,
01-0CT-2003 (TrEMBLrel. 25,
Amino acid ABC transporter,
                                                                                                                                                                                                                                                                                                                            90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 293:498-506(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPBIPQVLHAVG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 ALEKVNLGYLDLEQKIYTLSGGEAQRVALAKTILKNPPLILADEPTAALDPENSEEVMNL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 -LESFE-----EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21429245; PubMed=11544234;
Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHockins J., Alborn W.E. Jr., Arnold J., Fuller W., Geringer C., Gilmour R., Glass J.S., Knoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAbren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10; Gaps
    ., Hollingshead S.K., Fraser C.M.; a virulent isolate of Streptococcus
                                                                                                                                                                    GO, GO:0016020; C:membrane; IEA.
GO; GO:0016020; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0006610; P:ATP-binding; IEA.
GO; GO:0006610; P:TEAINBORT! IEA.
INTERFO; IPRO03439; ABC_transporter.
Pfam; PF00000; ABC_transporter.
ProDm; PR000006; ABC_transporter; I.
PROSITE; PS00211; ABC_TRANSPORTER_1; I.
PROSITE; PS002011; ABC_TRANSPORTER_2; I.
ATP-binding; Complete protecme.
SEQUENCE 213 AA; 23920 MW; F6BE2EA4EE87FDB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 39.2%; Score 399; DB 16; Length 213; Local Similarity 42.9%; Pred. No. 7.9e-25; les 90; Conservative 40; Mismatches 70; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MCT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter ATP-binding protein-unknown substrate.
ABC-NBD OR SPR1801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 LVDLKDENRIIIIATHNPLVWNKADEIIDM 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 LRALADKGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
         B.A., Morrison D.A.
                           "Complete genome sequence of
                                                                                   EMBL, AE007488; AAK76054.1;
PIR, E95232; E95232.
PIR, G98096; G98096.
                                                                   Science 293:498-506(2001),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=171101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                  TIGR; SP1987;
GO; GO:0016020;
GO; GO:0005524;
                                                 oneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
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61 EDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEIPQVLHAVG 120 121 -LESFE-----EKPVFELSGGEQORTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173 9 9 TIGR; SP0111; -.

Oct Go.0016620; C:membrane; IEA...

GO; GO.0016620; F:ATP binding; IEA...

GO; GO:000166; F:ATP-binding cassette (ABC) transporter acti. . .; IEA...

GO; GO:000166; F:nucleotide binding; IEA...

GO; GO:000166; F:nucleotide binding; IEA...

InterPro; IPR003593; AAA ATPASe...

InterPro; IPR003439; ABC\_transporter.

Pfam; PF00005; ABC\_tran; 1. 1 MIEINDLKKSFGVRILWOGLSHKFLPGTWTALTGASGSGKSTLLNCLGTLDKPSSGQILV Gaps

61 FGÇINLAVNSAKSÇIIIREHISYLFÇNFALIDDETVEYNIMLALKYVKLPKKÜKKVEE 120 61 BDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKPNLQLAV-----EKHKWPEIPQ 114 115 VLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEAL 174 1 MIBLKNITKTIGGKVILDNLSLRIDQGDLVAIVGKSGSGKSTLLNLLGLIDGDYSGRYEI 60 1 MIEINDLKKSFGVRILWOGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60 MEDLINE=21429245; PubMed=11544334; Blaszczak L.C., Burgett S., Hoskins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., Hoskins J., Alborn W.E. Jr., Fritz L., Fu D.-J., Fuller W., Geringer C., Gilmour R., Glass J.S., Khoja H., Kraft A.R., Lagace R.E., LeBlanc D.J. Lee L.N., Lefkowitz E.J., Lu J., Matushima P., Mcchren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Glass J.I., "Genome of the bacterium Streptococcus pneumoniae strain R6.";
J. Bacteriol. 183:5709-5717(2001).

R. Bacteriol. 183:5709-5717(2001).

R. BERL, ARC08933; AAK98904.1;
R. BOTS DAY884; D97884.

R. GO; GO:0016020; C:membrane; IEA.

R. GO; GO:0005524; F:ATP binding; IEA.

R. GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti...;

R. GO; GO:000166; F:TATP-binding cassette.

R. GO; GO:000166; F:TATP-binding cassette.

R. GO; GO:000166; F:TATP-binding cassette.

R. GO; GO:000166; F:TATP-binding cassette.

R. GO; GO:0000166; F:TATP-binding cassette.

R. DI-C-Pro; IPR003593; AAA ATP-ase.

R. DI-C-Pro; IPR003493; ABC\_transporter.

R. Prodom; PD000006; ABC transporter; 1.

R. PRODOM; PD00006; ABC transporter; 1. 9 Length 213; 01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter ATP-binding protein-amino acid transport.
ABC NBD OR SPR0100.
Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; 74; Indels Prodom; PD000006; ABC transporter; 1.
SMART; SM00382; AAA; I.
PROSITE; PS00211; ABC TRANSPORTER 1; 1.
PROSITE; PS0393; ABC TRANSPORTER 2; 1.
ATP-binding; Complete proteome.
SEQUENCE 213 AA; 23640 MW; E3E696AEB3677399 CRC64; PROSITE; PS00211; ABC\_TRANSPORTER\_1; 1.
PROSITE; PS50893; ABC\_TRANSPORTER\_2; 1.
ATP-binding; Complete\_Proceome.
SEQUENCE 213 AA; 23626 WW; 20E696AEB367738B CRC64; 37.9%; Score 386; DB 16; 40.2%; Pred. No. 9.2e-24; tive 45; Mismatches 74; 175 RALADKGATVVVATHSPLFRESADTIIKL 203 181 LEMNREGKTVIIVTHDAYVAQQCHRIIEL 209 Query Match
Best Local Similarity 40.2' PRELIMINARY; NCBI\_TaxID=171101; Q8DRI7 Q8DRI7; 8 8 8 8 8 8 8 8 8 8 8 8 g 셤 g a ò 8 ò

DB 16;

Score 385;

37.8%;

61 FGQINLAVNSAKSQTIIREHISYLFQNFALIDDETVEYNIMLALKYVKLPKKUKKVEE 120 61 EDVDLLKLSTRKORLYRKNTVGYLFQDYALIPDRTVKFNLQLAV----EKHKWPEI--PQ 114 115 VLHAVGLESFE-EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173 118 ALSKVGLENYNIDRKIFSLSGGEAQRVAIAKLIIKSPPIILADEPTGSLDRETGKEVMDI 177 61 EDVDLLKLSTRKORLYRKNIVGYLFQDYALIPDRTVKFNLQLAV-----BKHKWPEIPQ 114 115 VLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEAL 174 9 9 1 MIEINDLKKSFGVRILWOGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60 STATINITED FIRE 972;

RA Sanchez C., Hernandez de Rojas A., Martinez B., Arguelles M.E.,
RA Suarez J.E., Rodriguez A., Mayo B.;
Suarez J.E., Rodriguez A., Mayo B.;
Suarez J.E., Rodriguez A., Mayo B.;
Suarez J.E., Rodriguez A., Mayo B.;
Inactococcus lactis IPLA 972.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-!— SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.

BR GO; GO:0046821; C:extrachromosomal DNA; IEA.

BR GO; GO:0016620; C:membrane; IEA.

BR GO; GO:0005524; F:ATP-binding cassette (ABC) transporter acti. .; IEA

GO; GO:000166; F:nuclectide binding; IEA.

BR GO; GO:000166; F:nuclectide binding; IEA.

BR GO; GO:0005539; AAA\_ATPase.

BINEERPEC; IPRO0359; AAA\_ATPase.

BINEERPEC; IPRO0359; AAA\_ATPASE.

BR ProDom; PD000006; ABC transporter;
BR PROSITE; PS00821; AAC TRANSPORTER 1;
BR PROSITE; PS00821; AAC TRANSPORTER 1;
BR PROSITE; PS00831; AAC TRANSPORTER 1;
BR PROSITE; PS00831; AAC TRANSPORTER 2;
BR ATP-binding; Transport; BR ATP-Binding; Transport; BR ATP-Binding; Transport; BR ATP-Binding; Transport; BR ATP-Binding; Transport; BR ATP-Binding; Transport; BR ATP-Binding; Transport; BR ATP-BINDING; BR ATP-BINDING; BR ATP-BINDING; BR ATP-BINDING; BR ATP-BINDING; BR ATP-BINDI 1 MIEINDLKKSFGVRILMQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV Bacteria, Firmicutes, Lactobacillales, Streptococcaceae, Lactococcus. NCBI\_TaxID=1360; 10; Q9L650; 01-0CT-2000 (TrEMBLrel. 15, Created) 01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical ATP binding protein. Lactococcus lactis (subsp. lactis) (Streptococcus lactis). 37.5%; Score 382; DB 2; Length 207 41.0%; Pred. No. 1.9e-23; tive 46; Mismatches 68; Indels 39.7%; Pred. No. 1.1e-23; sive 46; Mismatches 74; Indels 175 RALADKGATVVVATHSPLFRESADTIIKL 203 0.0 Query Match
Best Local Similarity 41.09
Matches 86; Conservative | Similarity 39.7 83; Conservative PRELIMINARY; SEQUENCE FROM N.A. Best Local Matches 8 RESULT . SOW REPRESENTATION OF THE PROPERTY OF THE PROP 셤 ð g ò g  $\dot{\delta}$ ò d ò

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177 LLSLRDDNRLIIIATHNPAIWEMADEVFTM 206
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                                                                                                                                                                                Streptococcus
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                                                               Q8DNF2
                                      RESULT 12
Q8DNF2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 EDVDLLKLSTRKQRLYRKMTVGYLFQDYALIPDRTVKFNLQLAVEKHKWPEI-----PQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 VLHAVGLESFE-EKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSELVIEA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GO, GO: 0016620; C: membrane; IEA.
GO; GO: 0016524; F.ATP-binding; IEA.
GO; GO: 0004009; F.ATP-binding cassette (ABC) transporter acti...; IEA.
GO; GO: 0003677; F: DNA binding; IEA.
GO; GO: 0003170; F: N-membry Lransferase activity; IEA.
GO; GO: 0006106; P: N-methylation; IEA.
GO; GO: 0006106; P: N-methylation; IEA.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR003622; N6_Mtase.
PF00005; ABC_tran; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MIEINDLKKSFGVRILWQGLSHKFLPGTMTALTGASGSGKSTLLNCLGTLDKPSSGQILV 60
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                                                                                                                                                                                                                                                                   STRAIN=ATCC BAA-34 / TIGR4;
MEDLINE=21357209; PubMed=11463916;
MEDLINE=21357209; PubMed=11463916;
Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
Holtzapple B., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
Holt I.E., Loftus B.J., Yang F., Smith H.O., Veneer J. C.,
Complete genome sequence of a virulent isolate of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 11; Gaps
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                                                                                                                                                                                                      Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 AA; 23751 MW; EC0373F9E66FE167 CRC64;
                                                                                                                   01-0cT-2001 (TrEMBLrel. 18, Created)
01-0cT-2001 (TrEMBLrel. 18, Last sequence update)
01-0cT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter, ATP-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.3%; Score 380.5; DB 16;
41.0%; Pred. No. 2.5e-23;
ative 41; Mismatches 72;
                                                                                                      210 AA.
            LRALADKGATVVVATHSPLFRESADTIIKL 203
                           174 LRALADKGATVVVATHSPLFRESADTIIKL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00005; ABC_tran; 1.
ProDom; PD000006; ABC_transporter; 1.
PROSITE; PS00211; ABC_TRANSPORTER 1; 1.
PROSITE; PS50893; ABC_TRANSPORTER 2; 1.
PROSITE; PS00092; NG_MTASE; 1.
                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                        Science 293:498-506(2001).
EMBL, AE007485; AAK76024.1; -.
PIR, C98093, C98093.
TIGR, SP1957; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 41.0%
Matches 86; Conservative
                                                                                                                                                                                              Streptococcus pneumoniae.
                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Complete
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                   NCBI_TaxID=1313;
                                                                                                                                                                                                                     Streptococcus
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            174
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                                                                        RESULT 11
Q97NR1
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117 ALEQVGLVYLDLDKRIFELSGGESGRVALAKIILKNPPFILADEPTASIDPATSQLIMEI 176
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GO; GO:0005524; F:ATP-binding; IEA.

GO; GO:0005524; F:ATP-binding cassette (ABC) transporter acti. . ; IEA.

GO; GO:0003677; F:DN binding; IEA.

GO; GO:0000170; F:N-methyltransferase activity; IEA.

GO; GO:0000170; F:N-methyltransferase activity; IEA.

GO; GO:0000306; F:NDR methylation; IEA.

GO; GO:0006306; P:NDR methylation; IEA.

InterPro; IPR003593; AAA_ATPase.

InterPro; IPR003593; AAA_ATPase.

InterPro; IPR003593; AAA_ATPase.

InterPro; IPR00365; ABC_transporter.

Probon; PD00006; ABC_transporter; I.

SWART; SM00382; AAA; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDILINE-2192045; PubMed=11544234;
MEDILINE-2192045; PubMed=11544234;
DeHostins J., Alborn W.E. Jr., Arnold J., Blaszczak L.C., Burgett S., DeHostins J., Alborn W.E.
Gilmour R., Glass J.S., Rhoja H., Kraft A.R., Lagace R.E.,
Gilmour R., Glass J.S., Rhoja H., Kraft A.R., Lagace R.E.,
McAhren S.M., McHenney M., McLeaster K., Mundy C.W., Nicas T.I.,
Nortis F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P.,
Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G.,
Zook C.A., Baltz R.H., Jaskunas S.R., Rosteck P.R. Jr., Skatrud P.L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 EDVDLLKLSTRKORLYRKNTVGYLFQDYALIPDRTVKFNLOLAVEKHKWPEI-----PQ
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"Genome of the bacterium Streptococcus pneumoniae strain R6.";
J. Bacteriol. 183:5709-5717(2001).
EMBL, AE008541; AAL00576.1;
PIR, C98093; C98093.
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                                                                                                                                                                                                                                                                                 Streptococcus pneumoniae (strain ATCC BAA-255 / R6).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae;
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PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
PROSITE; PS50893; NG_MTABS; 1.
ATP-binding; Complete proteome.
SEQUENCE 210 AA; 23751 MW; EC0373F9E66FE167 CRC64;
                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter ATP-binding protein-unknown substrate.
ABC-NBD 08 SPR1773
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PRELIMINARY;
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SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
STRAIN=C-125 / JCM 9153;
STRAIN=C-20512582;
Pubmed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Puji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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36.8%; Score 375; DB 16; Length 22
Best Local Similarity 38.1%; Pred. No. 7.9e-23;
Matches 82; Conservative 46; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
PROSITE; PS5083; ABC_TRANSPORTER_2; 1.
ATP-binding; Complete_proceome.
ATP-binding; Complete_proceome.
Z28 AA; Z5261 WW; E8D6912DC95BA631 CRC64;
                                                                                                                                 (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                        ABC transporter (ATP-binding protein)
BH3505.
                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                    Bacillus halodurans
                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=86665;
                                                                                                                                     01-OCT-2000
01-OCT-2000
01-OCT-2003
                                                                    09K767
RESULT 13
                                                                        DDA KKRY COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON THE COOS ON T
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109 WPEIPQVLHAVGLESFEEKPVFELSGGEQQRTALARVLLKNPRIILADEPTGALDLTNSE 168
                                                                                                                                                                       57 QILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFNLQLAV------EKHK 108
                             26
                                                1 MIQLEGITKTFNTNAVSFQALNNVSLSIKEGEFVAITGTSGSGKTTLLNILGCLDDPTSG 60
                             1 MIBINDLKKSFGVR-ILWQGLSHKFL---PGTMTALTGASGSGKSTLLNCLGTLDKPSSG
Gaps
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Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firm.cutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBL_TaxID=1360;
                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ABC transporter ATP-binding protein.
                              PRELIMINARY;
                              09CJI3
RESULT 14
Q9CJI3
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181 EIMEILNKLHKEGKTVIIVTHDPFVADYCDRIIQL 215

[2] SEQUENCE FROM N.A.

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A MADINEALIZES186; Pubmed=1133/4/17

A MADINEALIZES186; Pubmed=1133/4/17

B Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K.,

Neissenbach J., Ehrlich S.D., Sorokin A.;

The complete genome sequence of the lactic acid bacterium Lactococcus

The complete genome sequence of the lactic acid bacterium Lactococcus

The complete genome sequence of the lactic acid bacterium Lactococcus

The complete genome sequence of the lactic acid bacterium Lactococcus

The complete genome sequence of the lactic acid bacterium Lactococcus

The complete genome sequence of the lactic acid bacterium Lactococcus

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 115 VLHAVGLESFEEKPVFELSGGEQORTALARVLLKNPRIILADEPTGALDLTNSELVIEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36.6%; Score 373; DB 16; Length 2
39.2%; Pred. No. 1.1e-22;
iive 42; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 RALADKGATVVVATHSPLFRESADTIIKL
                                                                                     MEDLINE=21235186; PubMed=11337471;
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SEQUENCE FROW N.A.
SEQUENCE FROW N.A.
STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
MEDLINE=21477403; PubMed=11579248;
OMUTE S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
"Genome sequence of an industrial microorganism Streptomyces
avermitilis: Deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
NCBI_TaxID=33903;
                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001)
                                                                                                                                                                                                     01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 25, Last sec
01-OCT-2003 (TrEMBLrel. 25, Last ant
ABC transporter ATP-binding protein.
                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Streptomyces avermitilis.
                                                                                                        PRELIMINARY;
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57 QILVEDVDLLKLSTRKQRLYRKNTVGYLFQDYALIPDRTVKFN----LQLAVEKHKWPEI 112
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Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
Sakaki Y., Hattori M., Omura S.;
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